

GenCore version 5.1.1.6
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OM protein - protein search, using sw model
Run on: March 12, 2005, 04:53:02 ; Search time 26.1438 Seconds
(without alignments)
614.609 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWGTLGGFLWLPYFYVQ.....SRLOGLQDMLWQLDLSGPC 167

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	167	1 LTHU	leptin precursor -
2	854.5	98.2	166	2 I53166	leptin precursor -
3	704	80.9	167	1 LTHS	leptin precursor -
4	690	79.3	167	1 LTRT	leptin precursor -
5	690	78.3	167	2 I55622	rat ob - rat
6	84	9.7	639	2 A10055	probable soluble 1
7	81.5	9.4	226	2 A1868	hypothetical prote
8	81.5	9.4	1600	2 AB3281	glutamate dehydrog
9	81	9.3	462	2 JCS625	14-nm filament pro
10	80.5	9.3	444	2 S54039	hypothetical prote
11	79.5	9.1	296	2 D8511	ATP-dependent RNA
12	79.5	9.1	696	2 S44912	hypothetical prote
13	79	9.1	409	2 B89954	hypothetical prote
14	79	9.1	829	2 T01362	probable myosin he
15	79	9.1	952	2 H84583	hypothetical prote
16	79	9.1	1364	2 T40839	hypothetical prote
17	78	9.0	420	2 S75514	sensory transducti
18	78	9.0	421	2 AB2959	exopolysaccharide
19	78	9.0	423	2 D98324	exopolysaccharide
20	78	9.0	2513	2 G96536	hypothetical prote
21	77.5	8.9	460	2 F90097	hypothetical prote
22	77.5	8.9	574	1 B42374	phosphotransferase
23	77.5	8.9	1036	2 D70117	acriflavine resist
24	77	8.9	628	2 A82889	hypothetical prote
25	76.5	8.8	173	2 S77486	ribosomal protein
26	76.5	8.8	362	2 A83967	carbamoyl-phosphat
27	76.5	8.8	600	2 AE0233	lipoprotein inner
28	76.5	8.8	600	2 T47045	hypothetical prote
29	76.5	8.8	600	2 T17437	ybcP protein - Yer

30	76.5	8.8	674	2 S46092	probable membrane
31	76.5	8.8	822	2 E86305	probable trehalose
32	76	8.7	142	2 C72430	hypothetical prote
33	76	8.7	327	2 AH2312	glycine cleavage r
34	76	8.7	570	2 T46011	hypothetical prote
35	76	8.7	995	2 H59432	RhOGAP protein hom
36	75.5	8.7	403	2 T36551	hypothetical prote
37	75.5	8.7	845	2 H13117	probable methyl-ac
38	75.5	8.7	1438	2 D59792	probable membrane
39	75	8.6	296	2 D70424	5,10-methylenetet
40	75	8.6	424	2 E81358	glutamate-1-semial
41	75	8.6	790	2 H71509	phenylalanine-tRNA
42	75	8.6	1191	2 S76414	beta transducin-li
43	74.5	8.6	534	2 B69896	methyl-accepting c
44	74.5	8.6	559	2 AB2202	hypothetical prote
45	74	8.5	177	2 A28106	prolactin, 20K - M

ALIGNMENTS

RESULT 1

LTHU
leptin precursor - human
N/Alternate names: obese protein; obesity factor
C/Species: Homo sapiens (man)
C/Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C/Accession: A38952; J00148
R/Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A/Title: Positional cloning of the mouse obese gene and its human homologue.
A/Reference number: S50863; MUID:95075453; PMID:7984236
A/Accession: A38952
A/Status: preliminary; nucleic acid sequence not shown
A/Molecule type: mRNA
A/Residues: 1-167 <ZHA>
A/Cross-references: UNIPROT:P41159; GB:U18915; NID:9623331; PIDN:AAA60470.1; PID:962333.
R/Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A/Title: Cloning of Chinese obesity gene and construction of prokaryotic expression vec
A/Reference number: J00148
A/Accession: J00148
A/Molecule type: mRNA
A/Residues: 'M', 22-167 <LIA>
A/Experimental source: adipose
A/Note: the author translated GAC for residue 148 as Ser
C/Genetics:
A/Gene: GDB:LEP; OB; OBS
A/Cross-references: GDB:I36420; OMIM:164160
A/Map position: 7q31.3-7q31.3
C/Superfamily: leptin
C/Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 100.0%; Score 870; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.8e-70;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY	1	MHWGTLGGFLWLPYFYVQAVPIQKVODDTKTLKTVTRINDISHTQSVSSKQKVTGL	60
DB	1	MHWGTLGGFLWLPYFYVQAVPIQKVODDTKTLKTVTRINDISHTQSVSSKQKVTGL	60
QY	61	DFIPGLHPIILTLTKNDQTLAVYQQILTSWPSNRVIQISNDLENLRDLLHLVAFSSKCHLP	120
DB	61	DFIPGLHPIILTLTKNDQTLAVYQQILTSWPSNRVIQISNDLENLRDLLHLVAFSSKCHLP	120
QY	121	WASGLETLDSLGCVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC	167
DB	121	WASGLETLDSLGCVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC	167

RESULT 2

```
I53166
leptin precursor - human
N:Alternate names: obese
C:Species: Homo sapiens (man)
C:Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I53166; G02328
R:Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Ta
Diabetes 44, 855-858, 1995
A:Title: Human obese gene expression. Adipocyte-specific expression and regional differe
A:Reference number: I53166; MUID:95309556; PMID:7789654
A:Accession: I53166
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-166 <RES>
A:Cross-references: UNIPROT:P41159; GB:D49487; NID:G904211; PIDN:BAA08448.1; PID:G904212
R:Chehab, F.F.; Lim, M.E.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01063
A:Accession: G02328
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <CHE>
A:Cross-references: EMBL:U43415; NID:g1163105; PIDN:AAC31660.1; PID:g1163106
C:Genetics:
A:Gene: GDB:LEP; OB; OBS
A:Cross-references: GDB:136420; OMIM:164160
A:Map position: 7q32.1-7q32.1
A:Introns: 48/3
C:Superfamily: leptin

Query Match 98.2%; Score 854.5; DB 2; Length 166;
Best Local Similarity 99.4%; Pred. No. 4.3e-69;
Matches 166; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHT-SVSSKQKVTGL 59
QY 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENRLDLHLVLAFAKSKSLP 120
DB 60 DFIPGLHPILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENRLDLHLVLAFAKSKSLP 119
QY 121 WASGLETLDSLGVLASGYTEVVALSRQGSQDMLWQDLSPGC 167
DB 120 WASGLETLDSLGVLASGYTEVVALSRQGSQDMLWQDLSPGC 166

RESULT 3
LITMS
leptin precursor - mouse
N:Alternate names: obese protein
C:Species: Mus musculus (house mouse)
C:Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: S50863
R:Zhang, Y.; Froenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A:Title: Positional cloning of the mouse obese gene and its human homologue.
A:Reference number: S50863; MUID:95075453; PMID:7984236
A:Accession: S50863
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <ZHA>
A:Cross-references: UNIPROT:P41160; EMBL:U18812; NID:G746416; PIDN:AAA64564.1; PID:G6032
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 80.9%; Score 704; DB 1; Length 167;
Best Local Similarity 83.2%; Pred. No. 1.2e-55;
Matches 139; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
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DB 1 MCVRLCFLWLSYLVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVAKQRTGL 60
QY 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENRLDLHLVLAFAKSKSLP 120
DB 61 DFIPGLHPILTSKMDQTLAVYQQVLTSLPSONVLQIANDLENRLDLHLVLAFAKSKSLP 120
QY 121 WASGLETLDSLGVLASGYTEVVALSRQGSQDMLWQDLSPGC 167
DB 121 QTRGLQKPESLDGVLASGYTEVVALSRQGSQDILQQLDVSPEC 167

RESULT 4
LITRT
leptin precursor - rat
N:Alternate names: obese protein; obesity factor
C:Species: Rattus norvegicus (Norway rat)
C:Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: PC4034; JC4142
R:Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noza
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A:Title: Enhanced expression of rat obese (ob) gene in adipose tissues of ventromedial h
A:Reference number: PC4034; MUID:95314614; PMID:7794258
A:Accession: PC4034
A:Molecule type: mRNA
A:Residues: 1-167 <FUN>
A:Cross-references: UNIPROT:P50596
A:Experimental source: adipose tissue
A:Note: The authors translated the codon AAA for residue 32 as Thr
R:Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A:Title: Cloning of rat obese cDNA and its expression in obese rats.
A:Reference number: JC4142; MUID:95251725; PMID:7733988
A:Accession: JC4142
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <MUR>
A:Cross-references: DDBJ:D49653; NID:g995614; PIDN:BAA08529.1; PID:g995615
A:Experimental source: liver
C:Comment: This protein is proposed to function as part of a signalling pathway from adi
C:Genetics:
A:Gene: Obese
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 79.3%; Score 690; DB 1; Length 167;
Best Local Similarity 82.0%; Pred. No. 2.1e-54;
Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 MHWGTLGFLWLPYLVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MCVRLCFLWLSYLVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVARQRTGL 60
QY 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPNRNVIQISNDLENRLDLHLVLAFAKSKSLP 120
DB 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPNRNVIQIANDLENRLDLHLVLAFAKSKSLP 120
QY 121 WASGLETLDSLGVLASGYTEVVALSRQGSQDMLWQDLSPGC 167
DB 121 QTRGLQKPESLDGVLASGYTEVVALSRQGSQDILQQLDVSPEC 167

RESULT 5
I55622
rat ob - rat
C:Species: Rattus sp. (rat)
C:Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I55622
R:Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; Ta
J. Clin. Invest. 96, 1647-1652, 1995
A:Title: Molecular cloning of rat obese cDNA and augmented gene expression in genetically,
```

A:Reference number: I55622; MUID:95386724; PMID:7657834

A:Accession: I55622

A:Status: preliminary; translated from GB/EMBL/DBJ

A:Molecule type: mRNA

A:Residues: 1-167 <RES>

A:Cross-references: GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID:g1018991

C:Superfamily: leptrin

Query Match 79.3%; Score 690; DB 2; Length 167;
Best Local Similarity 82.0%; Pred. No. 2.1e-54;
Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

QY 1 MHMGTLCGFLWLPYFVQVAPVQVQVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60

DB 1 MCMPLCFLWLSYLSVQVAPVPIHKVQDDTKTIKTIIVTRINDISHTQSVARQVTGL 60

QY 61 DFIPGLHPIILSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVAFSSKCHLP 120

DB 61 DFIPGLHPIILSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVAFSSKCHLP 120

QY 121 WASGLETLDSGGVLEASGYSTEVVALSRLOGLQDMLQDLSPCC 167

DB 121 QTRGLQKPESLDGVLEASLYSTEVVALSRLOGLQDMLQDLSPCC 167

RESULT 6

A:Accession: A10055

C:Species: Yersinia pestis

C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004

C:Accession: A10055

R:Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B.

deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;

il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,

Nature 413, 523-527, 2001

A:Title: Genome sequence of Yersinia pestis, the causative agent of plague.

A:Reference number: AB0001; MUID:21470413; PMID:11586360

A:Accession: A10055

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-639 <KUR>

A:Cross-references: UNIPROT:Q6Z1P2; GB:AL590842; PIDN:CAC89308.1; PID:g15978544; GSPDB:C

C:Genetics:

A:Gene: YPO0452

C:Superfamily: soluble lytic transglycosylase

C:Keywords: glycosidase; hydrolase

Query Match 9.7%; Score 84; DB 2; Length 639;
Best Local Similarity 21.7%; Pred. No. 14;
Matches 38; Conservative 22; Mismatches 41; Indels 74; Gaps 6;

QY 12 LWPYLYVQVAPVQVQVDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPIIL 71

DB 59 LYPYLYEQQL-----TQDLQVSTAQVKDFL-NRHPTLP 91

QY 72 LSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVAFSSKCHLP----- 120

DB 92 PAK-----SLPSRFV-----NELARREDWRGLTFTSPAPKPVAAACNYYVAK 134

QY 121 WASGLETL-----DSLGGVLEASGYSTEVVALSRLOGLQD 156

DB 135 WATGQSVAWEGASIWINGQSLPGSCDKLFSVWQQAQHTPLATLARKKALKE 189

RESULT 7

A:Accession: A1868

C:Species: Nostoc sp. PCC 7120

A:Note: Nostoc sp. strain PCC 7120 is a synonym of Anabaena sp. strain PCC 7120

C:Date: 14-Dec-2001 #sequence_revision 14-Dec-2001 #text_change 09-Jul-2004

C:Accession: A1868

R:Kaneko, T.; Nakamura, Y.; Wolk, C.P.; Kuritz, T.; Sasamoto, S.; Watanabe, A.; Iriguchi,

Nakazaki, N.; Shimpo, S.; Sugimoto, M.; Takazawa, M.; Yamada, M.; Tabata, S

DNA Res. 8, 205-213, 2001

A:Title: Complete Genomic Sequence of the Filamentous Nitrogen-fixing Cyanobacterium Ana

A:Reference number: AB1807; MUID:21595285; PMID:11759840

A:Accession: A1868

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-226 <KUR>

A:Cross-references: UNIPROT:Q8YZG8; GB:BA000019; PIDN:BAW7450.1; PID:g17129837; GSPDB:B

A:Experimental source: strain PCC 7120

C:Genetics:

A:Gene: all0492

C:Superfamily: Escherichia coli ygiH protein

Query Match 9.4%; Score 81.5; DB 2; Length 226;
Best Local Similarity 21.8%; Pred. No. 6.1;
Matches 41; Conservative 32; Mismatches 70; Indels 45; Gaps 6;

QY 3 WGTLCGFLWLPYLF-----YVQVAPVQVQVDDTKTIKTIIVTRINDISHTQSV 51

DB 4 WLSGCAVVLVAYLLGSPPTGYIAVKQKGDIDREVSGS-----TGATNVLRITLQK 55

QY 52 SSOKQVTDLPFIPGLHPIILTSKMDQTLAVYQQILTSMPSRNVIQISNDLE-----NL 104

DB 56 GPGAFVLGLDCLKGV-----LATAVYVLFYFASQNLIPPTVNIELWQPLVTL 105

QY 105 RDLHLVAFSSKCHLPWASGLETLDSGGVLEAS-----GYSTEVVALSRLOGLQD 156

DB 106 AGIAAILGHSKSIIFLFTGKSVATSLGILLAMNQVGLATFGVFAVVVAISRIV-SLS 164

QY 157 MLMQDLDS 164

DB 165 IMGAIASV 172

RESULT 8

AB3281

C:Species: Brucella melitensis

C:Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004

C:Accession: AB3281

R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Loe, T.; Ivanova,

Mazur, M.; Coleman, E.; Selkov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letes,

Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002

A:Title: The genome sequence of the facultative intracellular pathogen Brucella meliten

A:Reference number: AD3252; PMID:11756688

A:Accession: AB3281

A:Status: preliminary

A:Molecule type: DNA

A:Residues: 1-1600 <KUR>

A:Cross-references: UNIPROT:Q8YJ55; GB:AE008917; PIDN:AAL51413.1; PID:g17982118; GSPDB:B

A:Experimental source: strain 16M

C:Genetics:

A:Gene: BMEI0231

A:Map position: I

C:Keywords: oxidoreductase

Query Match 9.4%; Score 81.5; DB 2; Length 1600;
Best Local Similarity 24.6%; Pred. No. 76;
Matches 32; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

QY 27 VDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPIILTSKMDQTLAVYQQIL 86

DB 97 VNDNMPFLDSIMGELND--HTSQI-----FMVHVLDSIRKDELVLGEAS 143

QY 87 TSPSRNVIQISNDLENLRLDLHLVAFSSKCHLPWASGLETLDSGGVLEASGYSTEVVA 146

DB 144 QLAPANGVERVS-----LVQIHLPALSKQAKADTAGLKRV--LQOV--RRAVSDWKPM 193

QY 147 LSRLQGSLOD 156

DB 194 LKRLDGAIDD 203

RESULT 12
S44912
hypothetical protein ZK686.2 - Caenorhabditis elegans
N:Contains: hypothetical protein Z97.2
C:Species: Caenorhabditis elegans
C:Date: 20-Feb-1995 #sequence_revision 20-Feb-1995 #text_change 09-Jul-2004
C:Accession: S44912; S44884
R;Du, Z.
submitted to the EMBL Data Library, June 1993
A:Description: Sequence of the C. elegans cosmid ZK686.
A:Reference number: S44909
A:Accession: S44912
A:Molecule type: DNA
A:Residues: 1-696 <DUZ>
A:Cross-references: UNIPROT:P34668; EMBL:L117337; NID:G304345; PIDN:AAA28223.1; PID:G3043
A:Experimental source: cosmid ZK686
R;Du, Z.
submitted to the EMBL Data Library, May 1993
A:Description: Sequence of the C. elegans cosmid ZC97.
A:Reference number: S44615
A:Accession: S44884
A:Molecule type: DNA
A:Residues: 401-696 <DUW>
A:Cross-references: EMBL:L14714; NID:Q289737; PIDN:AAA28179.1; PID:Q289738
A:Experimental source: cosmid ZC97
A:Note: designated as ZC97.2 protein
C:Genetics:
A:Introns: 15/1; 89/3; 102/3; 120/3; 145/3; 194/2; 312/2; 453/3; 643/2
C:Keywords: ANP; nucleotide binding; P-loop
F;266-273/Region: nucleotide-binding motif A (P-loop)
F;373-378/Region: nucleotide-binding motif B
F;377-380/Region: DEAD motif
F;401-696/Product: hypothetical protein ZC97.2 #status predicted <ZCP>

Query Match 9.1%; Score 79.5; DB 2; Length 696;
Best Local Similarity 29.2%; Pred. No. 39;
Matches 33; Conservative 12; Mismatches 31; Indels 37; Gaps 6;

Qy 10 LWLW----PYLYVQVAVPIQKVDQDTKTIKTIIVTRINDISHT-----QSVSSKOKVT 58
Db 433 LHLWNLKPRLPFSATVS-----VKDITSGIPQVDHVSGRALPSSISHRLVVT 481

Qy 59 GLDFIPGLPILTLKMDQTLAVYQQLTSMPSRNVIQISNDLENLRDLHLVL 111
Db 482 D----PKFHP-----LAVIQITRNKFNRTLIFV-NEVSSNRLAHLV 519

RESULT 13
B89954
hypothetical protein SAI524 [imported] - Staphylococcus aureus (strain N315)
C:Species: Staphylococcus aureus
C:Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C:Accession: B89954
R;Kuroda, M.; Ohta, T.; Uchiyama, I.; Baba, T.; Yuzawa, H.; Kobayashi, I.; Cui, L.; Oguc
ma, A.; Mitutani-Ui, Y.; Kobayashi, N.; Sawano, T.; Inoue, R.; Kaito, C.; Sekimizu, K.;
C.; Shiba, T.; Hattori, M.; Ogasawara, N.; Hayashi, H.; Hiramatsu, K.
Lancet 357, 1225-1240, 2001
A:Title: Whole genome sequencing of methicillin-resistant Staphylococcus aureus.
A:Reference number: B89758; MUID:21311952; PMID:11418146
A:Accession: B89954
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-409 <KUR>
A:Cross-references: UNIPROT:Q99TG1; GB:BA000018; PID:gl3701497; PIDN:BAB42791.1; GSPDB:C
A:Experimental source: strain N315
C:Genetics:
A:Gene: SAI524
C:Superfamily: malate dehydrogenase (oxaloacetate-decarboxylating)

Query Match 9.1%; Score 79; DB 2; Length 409;
Best Local Similarity 21.3%; Pred. No. 22;
Matches 38; Conservative 36; Mismatches 56; Indels 48; Gaps 8;

Qy 19 VOAVPIQKVDQDTKTIKTIIV-----TRINDISHTQSVSSKOKVTGLDFIPGLH--- 67
Db 101 INGVPALNTTDTTEIIKTVKLEPNYGGINLEDSAPRCFEIIBERLKKETNPVPVHDDQ 160

Qy 68 ---PILTLKMDQTLAVYQQLTSMPSRNVIQISNDLENLRDLHL-----VLAFSKSCHL 119
Db 161 HGTAIVTMAGLVNALRV-----VNKDIKIKVVLNGAGAAGIAIVK---L 202

Qy 120 PWASGLETL---DSLGGVLEASGY---STEVVA-----LSRLQGSLOQMLQOLDLSPG 166
Db 203 LYAYGVNVMWCDRSGAIFEGRSYGMNPTKDVAKWTNKDKIEGSLSEVVKDADVFIG 260

RESULT 14
T01362
probable myosin heavy chain At2g34730 - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01362; C84760
R;Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kaul
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: Z14179
A:Accession: T01362
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <ROU>
A:Cross-references: UNIPROT:O64584; EMBL:AC003096; NID:g3132469; PID:g3132472
A:Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
Nature 402, 761-768, 1999
A:Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A:Reference number: B84420; MUID:20083487; PMID:10617197
A:Accession: C84760
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-829 <STO>
A:Cross-references: GB:AE002093; NID:g3132472; PIDN:AAC16261.1; GSPDB:GN00139
C:Genetics:
A:Gene: At2g34730; T29F13.6
A:Map position: 2
A:Introns: 728/2; 770/3

Query Match 9.1%; Score 79; DB 2; Length 829;
Best Local Similarity 21.5%; Pred. No. 54;
Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6;

Qy 24 IQKVQDDTKTIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLKMDQTLAVY- 82
Db 57 ISRVVSD--SIIRGWMTAIES-----DAAEKIAQKD-----LELSKIRETLILYH 99

Qy 83 -----QQLITMPSRNVIQISNDLENLRDLHLVLAFSKSCHLP 120
Db 100 VGSBENESSESLIHDELITQGSSESKKKAKQKQLMLVEELTNLREYTHIN----- 150

Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGLQDML 158
Db 151 -GSGATVDDSLG--LDSSPHETRSKTVDMKLDLSKSL 185

RESULT 15
H84583
hypothetical protein At2g20010 [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C:Accession: H84583
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.

GenCore version 5.1.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:03 ; Search time 124.85 Seconds
(without alignments)
517.333 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWTGTCFLWLPYFYVQ.....SRQGSLOQMLWQLDLSPGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04:*

- 1: _geneseqp1980s:*
- 2: _geneseqp1990s:*
- 3: _geneseqp2000s:*
- 4: _geneseqp2001s:*
- 5: _geneseqp2002s:*
- 6: _geneseqp2003as:*
- 7: _geneseqp2003bs:*
- 8: _geneseqp2004s:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	167	2 AAW03694	AAW03694 Human obe
2	870	100.0	167	2 AAR99473	AAR99473 Human obe
3	870	100.0	167	2 AAR92720	AAR92720 Obesity p
4	870	100.0	167	2 AAW34060	AAW34060 Human obe
5	870	100.0	167	2 AAW57442	AAW57442 Human lep
6	870	100.0	167	3 AAY82110	AAY82110 Human obe
7	870	100.0	167	3 AAB28448	AAB28448 Human OB
8	870	100.0	167	3 AAY84190	AAY84190 Amino aci
9	870	100.0	167	3 AAY80259	AAY80259 Human obe
10	870	100.0	167	3 AAY87726	AAY87726 Murine OB
11	870	100.0	167	3 AAB28467	AAB28467 Human OB
12	870	100.0	167	4 AAB59914	AAB59914 Human lep
13	870	100.0	167	4 AAB72927	AAB72927 Human lep
14	870	100.0	167	4 AAE10338	AAE10338 Human lep
15	870	100.0	167	4 AAU02890	AAU02890 Human Ob
16	870	100.0	167	4 AAB70128	AAB70128 Human lep
17	870	100.0	167	5 ABG74164	ABG74164 Human obe
18	870	100.0	167	5 ABB84116	ABB84116 Human obe
19	870	100.0	167	6 ABU64561	ABU64561 Human obe
20	870	100.0	167	7 ADE56246	ADE56246 Human Pro
21	870	100.0	167	7 ADF15260	ADF15260 Human alb
22	870	100.0	167	7 ADF15253	ADF15253 Human alb
23	870	100.0	167	7 ADF15257	ADF15257 Human alb
24	870	100.0	167	7 ADF15259	ADF15259 Human alb
25	870	100.0	167	7 ADH21374	ADH21374 Human lep

26	870	100.0	167	7 ADH21373	Adh21373 Human lep
27	870	100.0	167	7 ADH21372	Adh21372 Human lep
28	870	100.0	167	7 ADH21371	Adh21371 Human lep
29	870	100.0	167	8 ADH17068	Adh17068 Human lep
30	870	100.0	167	8 ADK19923	Adk19923 Human lep
31	870	100.0	167	8 ADO24730	Ado24730 Human lep
32	870	100.0	167	8 ADO19663	Ado19663 Human sof
33	870	100.0	396	2 AAW10534	Aaw10534 Leptin 1-
34	870	100.0	396	2 AAW10535	Aaw10535 Leptin 1-
35	870	100.0	397	2 AAW22722	Aaw22722 Human obe
36	870	100.0	397	2 AAW24060	Aaw24060 Human obe
37	870	100.0	397	2 AAD29344	Ad229344 Human obe
38	870	100.0	397	7 ADC08948	Adc08948 Human OB
39	870	100.0	397	7 ADC78787	Adc78787 Human PRO
40	870	100.0	399	2 AAW10536	Aaw10536 Leptin 1-
41	870	100.0	401	2 AAW10537	Aaw10537 Leptin 1-
42	870	100.0	752	7 ADF15039	Adf15039 Human alb
43	870	100.0	752	7 ADH21302	Adh21302 Human alb
44	866	99.5	167	4 AAU02994	Aau02994 Human Ob
45	866	99.5	167	4 AAU02989	Aau02989 Human Ob

ALIGNMENTS

RESULT 1

AAW03694
ID AAW03694 standard; protein; 167 AA.

XX AC AAW03694;

XX DT 15-JUL-1997 (first entry)

XX DE Human obese (ob) protein.

XX KW Human; obese; ob; body; weight; modulation; defect; mutation; prevention;

XX KW interference; production; function; treatment; control; obesity; disease;

XX KW reduction; food intake; gain; mammal; type II; diabetes; mellitus;

XX KW hypertension; hyperlipidaemia; hyperlipidemia; identification; receptor.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT Peptide /label= sig_peptide

FT Peptide 22..167

FT Peptide /label= mat_peptide

XX EP741187-A2.

XX PD 06-NOV-1996.

XX PF 24-APR-1996; 96EP-00106408.

XX PR 05-MAY-1995; 95US-00435777.

XX PR 07-JUN-1995; 95US-00484629.

XX PA (HOFF) HOFFMANN LA ROCHE & CO AG F.

XX PI Campfield A, Devos R, Guisez Y;

XX DR WPI; 1996-487390/49.

XX DR N-PSDB; AAT42168.

XX PT New isolated human and murine obese proteins - and related DNA, used for

XX PT the treatment, prevention and control of obesity and associated diseases.

XX PS Claim 3; Page 28-29; 36pp; English.

XX CC The present sequence is the human obese (ob) protein, a body weight

XX CC modulator, which can be administered to patients suffering from ob gene

XX CC defects or mutations which prevent or interfere with its production

XX CC and/or function. The ob protein can be used to treat, prevent or control

CC obesity and associated diseases by reducing food intake and weight gain
 CC in mammals. It can also be used to treat related conditions such as type
 CC II diabetes mellitus, hypertension and hyperlipidaemia, and to identify
 CC ob protein receptors. The human ob gene was isolated by screening a
 CC lambda phage cDNA library, made from human adipocyte tissue derived RNA,
 CC with a murine ob gene obtained using the methods of Zhang, Y. et al.,
 CC Nature 372, 425-432 (1994)
 XX
 SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 DB 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 QY 61 DFIPGLHPILTSLKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 DB 61 DFIPGLHPILTSLKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 QY 121 WASGLETLDSLGVLASGYSTEVVALSRQGSLODMLWQDLSPGC 167
 DB 121 WASGLETLDSLGVLASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 2

AAR99473
 ID AAR99473 standard; protein; 167 AA.

XX AC AAR99473;
 XX DT 22-OCT-1996 (first entry)
 XX DE Human ob protein.
 XX KW Obesity; ob gene; ob protein; appetite suppression factor.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Peptide 1..21
 XX FT Protein /label= Sig_peptide
 XX FT Protein /label= Mat_protein
 XX W09622308-A2.

XX PD 25-JUL-1996.
 XX PF 22-JAN-1996; 96WO-US001471.
 XX PR 20-JAN-1995; 95US-00377068.
 XX PR 10-APR-1995; 95US-00419214.
 XX PR 07-JUN-1995; 95US-00486450.
 XX PR 07-JUN-1995; 95US-00486459.
 XX PR 07-JUN-1995; 95US-00487111.
 XX PR 04-OCT-1995; 95US-00540242.

XX (ZYMO) ZYMOGENETICS INC.
 XX (UNIW) UNIV WASHINGTON.

XX Weigle DS, Kuiper JL, Bukowski TR;
 XX WPI; 1996-354476/35.
 XX N-PSDB; AAT34164.

XX Identifying factors that regulate appetite, e.g. for treatment of obesity
 XX - by administering a test sample to a mammal and determining decrease in
 XX food consumption.

XX Claim 6; Page 76; 90pp; English.

XX The human ob protein (appetite suppression factor) amino acid sequence
 CC (AAR99473) was deduced from a cDNA clone (AAR34164) derived from human
 CC adipose tissue. The mature ob protein, pref. modified with an N-terminal
 CC histidine tag, can be obtd. by expression in transformed host (esp.
 CC yeast) cells. It is used to regulate the appetite of an individual,
 CC thereby decreasing food consumption. Mouse ob proteins (see also AAR99472
 CC and AAR99474) were also identified
 XX
 SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 DB 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKLIKIVTRINDISHTQSVSSKQKVTGL 60
 QY 61 DFIPGLHPILTSLKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 DB 61 DFIPGLHPILTSLKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 QY 121 WASGLETLDSLGVLASGYSTEVVALSRQGSLODMLWQDLSPGC 167
 DB 121 WASGLETLDSLGVLASGYSTEVVALSRQGSLODMLWQDLSPGC 167

RESULT 3

AAR92720
 ID AAR92720 standard; protein; 167 AA.

XX AC AAR92720;
 XX DT 12-SEP-1996 (first entry)
 XX DE Obesity protein.

XX KW Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
 XX food intake; energy expenditure; high blood pressure; cholesterol; human;
 XX Gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
 XX OS Homo sapiens.

XX FH Key Location/Qualifiers
 XX FT Peptide 1..21
 XX FT Protein /note= "signal peptide"
 XX FT Protein /note= "obesity protein"

XX GB2292382-A.
 XX PD 21-FEB-1996.

XX PF 17-AUG-1995; 95GB-00016947.
 XX PR 17-AUG-1994; 94US-00292345.
 XX PR 30-NOV-1994; 94US-00347563.
 XX PR 10-MAY-1995; 95US-00438431.
 XX PR 07-JUN-1995; 95US-00483211.

XX (UYRQ) UNIV ROCKEFELLER.

XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
 XX Burley SK;

XX WPI; 1996-099009/11.
 XX N-PSDB; AAT16373.

XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
 XX reducing wt. in treatment of diabetes, high blood pressure and high
 XX cholesterol and for cosmetic reasons.

XX

PS Claim 2; p171-172; 304pp; English.

XX This sequence represents the human obesity polypeptide (OBP). OBP (also known as leptin) is a hormone involved in the regulation of body weight.

CC This sequence has effects on both food intake and energy expenditure. OBP and its analogues are useful for modifying body weight (optionally combined with known medicaments), for treating diabetes, high blood pressure or high cholesterol. The DNA encoding this sequence (and sequences complementary to it) can be used in gene therapy for modifying body weight. This protein can be used for reducing weight for health or cosmetic reasons in obese humans, or to produce leaner food animals.

CC Antagonists of OBP (including antibodies) are useful for increasing body weight, e.g. for treating weight loss associated with cancer, or for cosmetic reasons in humans, or for production of Kobe beef or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP complexes enables in vitro evaluation of levels of OBP in a sample, especially to detect diseases associated with elevated or decreased levels, and to monitor treatment of these diseases

XX

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIFGLHPILTLKMDQTLAVYQOILTSMPGRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 Db 61 DFIFGLHPILTLKMDQTLAVYQOILTSMPGRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSFGC 167
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSFGC 167

RESULT 4
 AAW34060
 ID AAW34060 standard; protein; 167 AA.
 AC AAW34060;
 XX
 XX
 DT 24-APR-1998 (first entry)
 XX
 XX Human obese (ob) protein.
 DE
 KW Obese protein; ob protein; osteogenic cell; bone-forming activity; migration; bone-forming cell; marrow mesenchymal cell; bone repair; bone healing; bone loss.
 KW
 KW
 OS Homo sapiens.
 XX
 XX Key Location/Qualifiers
 FH Peptide 1..21
 FT /note= "signal peptide"
 XX
 XX WO9739767-A1.
 PN
 XX
 XX 30-OCT-1997.
 PD
 XX
 XX 18-APR-1997; 97WO-US006892.
 PP
 XX
 XX 19-APR-1996; 96US-0015647P.
 PR
 XX (ZYMO) ZYMOGENETICS INC.
 XX (UNIW) UNIV WASHINGTON.
 PA
 XX Durnam DM, Kuijper JL, Weigle DS, Liu CC;
 PI WPI; 1997-535577/49.
 XX

DR N-PSDB; AAT93021.

XX Use of obese protein for inducing bone formation - particularly for treating osteoporosis, repairing fractures, dental defects or resectioning due to oncogenesis.

PT

XX Disclosure; Page 32; 42pp; English.

PS

XX The present sequence represents a human obese (ob) protein. DNA sequence was isolated from an adipose tissue cDNA library using a probe derived from the mouse obese gene. ob proteins can produce a dramatic increase in osteogenic cells or their bone-forming activity. They can enhance recruitment or migration of bone-forming cells to the proper bone-forming tissues and tissue sites. The ob protein was used in the method of the invention, which involves the stimulation of a cell population containing marrow mesenchymal cells. The method comprises exposing the cell population to an ob protein for expansion of osteogenic cells, a biological fluid obtained from an ob protein-treated mammal, or a culture medium that has been conditioned by growth of endocrine or CNS cells or tissue exposed to ob protein. The method can be used in a mammal for promoting bone repair or bone healing, stimulating bone ingrowth into a prosthetic device or dental implant that has been inserted into a mammal, for treating bone loss, for increasing bone length, for stimulating active bone growth, or for inducing bone formation

XX

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60

Qy 61 DFIFGLHPILTLKMDQTLAVYQOILTSMPGRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
 Db 61 DFIFGLHPILTLKMDQTLAVYQOILTSMPGRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSFGC 167
 Db 121 WASGLETLDSLGGVLEASGYSTEVALSRQSLQSLQDMLWQLDLSFGC 167

RESULT 5
 AAW57442
 ID AAW57442 standard; peptide; 167 AA.
 AC AAW57442;
 XX
 XX
 DT 10-AUG-1998 (first entry)
 XX
 XX Human leptin sequence.
 DE
 XX Leptin; murine; antagonist; treatment; type II diabetes; insulin; human.
 KW
 XX Homo sapiens.
 OS
 XX Key Location/Qualifiers
 FH Disulfide-bond 7..167
 FT /note= "disulphide bridge"
 XX
 XX WO9812224-A1.
 PN
 XX
 XX 26-MAR-1998.
 PD
 XX
 XX 15-SEP-1997; 97WO-EP005035.
 PP
 XX
 XX 20-SEP-1996; 96DE-01038487.
 PR
 XX (FARH) HOECHST AG.
 PA
 XX Ertl J, Freibisch G, Mueller G;
 PI
 XX

XX WPI; 1998-217209/19.
 XX Use of leptin antagonists - for restoring or amplifying the physiological
 PT effect of insulin in the treatment of Type II diabetes.
 XX
 XX Disclosure; Page 19; 30pp; English.
 XX
 XX This is a human leptin protein sequence which is highly homologous to the
 CC murine leptin sequence. The carboxyl-terminal fragment of the murine
 CC leptin can act as a leptin antagonist. This can be used in a
 CC pharmaceutical composition which comprises the murine leptin fragment
 CC which is therapeutically beneficial for the treatment of Type II
 CC diabetes. The leptin antagonists include peptides derived from leptin
 CC fragments and may be obtained by chemically or enzymatically cleaving
 CC intact leptin or by recombinant expression using microorganisms. This
 CC fragment can be prepared by digestion of leptin with lysyl endopeptidase.
 CC The leptin antagonists can restore or amplify the physiological effect of
 CC insulin by inhibiting leptin-induced insulin resistance
 XX
 XX Sequence 167 AA;
 SQ
 Query Match 100.0%; Score 870; DB 2; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
 Qy 61 DFIPGLHPILTSLKMDQTLAVYQIILTMPSRNVQISNDLENLRLDLLHLVAFSKSCHLP 120
 Db 61 DFIPGLHPILTSLKMDQTLAVYQIILTMPSRNVQISNDLENLRLDLLHLVAFSKSCHLP 120
 Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
 Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
 RESULT 6
 AAY82110
 ID AAY82110 standard; protein; 167 AA.
 XX
 AC AAY82110;
 DT 05-JUN-2000 (first entry)
 DE Human obese protein SEQ ID NO:5.
 XX
 XX Ob gene; ob protein; obesity; body weight; polyethylene; obese protein;
 KW polypropylene; protein conjugate; anorectic.
 XX
 XX Homo sapiens.
 OS
 XX US6025324-A.
 PN
 XX 15-FEB-2000.
 PD
 XX 15-MAY-1996; 96US-00648262.
 PF
 XX 15-MAY-1996; 96US-00648262.
 PR
 XX (HOFF) HOFFMANN LA ROCHE INC.
 PA
 XX Bailon PS, Devos R, Campfield A, Guisez Y;
 PI
 XX WPI; 2000-222636/19.
 DR N-PSDB; AAZ95530.
 XX
 XX Polyethylene and polypropylene obese protein conjugates are useful for
 PT the prevention, treatment and control of obesity and associated diseases
 PT and conditions.
 XX

PS Disclosure; Col 35-36; 26pp; English.
 XX
 XX The present invention describes a composition comprising one or more
 CC polyethylene and polypropylene human obese protein conjugates (I). The
 CC composition has anorectic activity. The conjugates are used for the
 CC treatment, prevention and control of obesity and associated conditions in
 CC humans and animals. The present sequence represents the human obese
 CC protein
 XX
 XX Sequence 167 AA;
 SQ
 Query Match 100.0%; Score 870; DB 3; Length 167;
 Best Local Similarity 100.0%; Pred. No. 4.8e-85;
 Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
 Qy 61 DFIPGLHPILTSLKMDQTLAVYQIILTMPSRNVQISNDLENLRLDLLHLVAFSKSCHLP 120
 Db 61 DFIPGLHPILTSLKMDQTLAVYQIILTMPSRNVQISNDLENLRLDLLHLVAFSKSCHLP 120
 Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
 Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
 RESULT 7
 AAB28448
 ID AAB28448 standard; protein; 167 AA.
 XX
 AC AAB28448;
 DT 01-FEB-2001 (first entry)
 DE Human OB polypeptide.
 XX
 XX Human; mouse; OB gene; obesity; adiposity; body weight.
 KW
 XX Homo sapiens.
 OS
 XX US6124448-A.
 PN
 XX 26-SEP-2000.
 PD
 XX 07-JUN-1995; 95US-00488208.
 PF
 XX 17-AUG-1994; 94US-00292345.
 PR 30-NOV-1994; 94US-00347563.
 PR 10-MAY-1995; 95US-00438431.
 XX
 XX (UYRQ) UNIV ROCKEFELLER.
 PA
 XX Maffei M, Proenca R, Zhang Y, Friedman JM;
 PI
 XX WPI; 2000-601556/57.
 DR N-PSDB; AAC62566.
 XX
 XX Nucleic acid primers and probes useful for detecting mutations in
 PT mammalian OB gene associated with regulation of body weight and
 PT adiposity.
 XX
 XX Example; Fig 3; 153pp; English.
 PS
 XX The present sequence is encoded by a nucleotide sequence used in an
 CC invention relating to the control of body weight of animals including
 CC humans. Nucleic acids of at least 10 nucleotides which are hybridisable
 CC to a non-coding region of an OB nucleic acid have been created. The OB
 CC gene plays a critical role in the regulation of body weight and
 CC adiposity. The nucleic acids may be used as probes or as primers for PCR.
 CC They are useful for evaluating the presence of mutations in the human OB
 CC gene or for evaluating the level of expression of OB mRNA. Defects

CC associated with OB gene expression result in obese phenotypes
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIFGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLP 120
Db 61 DFIFGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSGPC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSGPC 167

RESULT 8
AAV84190
ID AAY84190 standard; protein; 167 AA.
XX
AC AAY84190;
XX

DT 03-JUL-2000 (first entry)
XX

DE Amino acid sequence of the primary structure of human leptin.
XX

XX Human; leptin; blood brain barrier; homeostasis; body mass; anorexia;
KW obesity; hyperglycemia; hyperinsulinemia; hyperphagia;
KW thyroid dysfunction; infertility; type II diabetes mellitus;
KW non-insulin-dependent diabetes mellitus; hematopoiesis dysfunction;
KW tumour suppression; weight loss; diet.
XX

OS Homo sapiens.
XX

PN WO200011173-A1.
XX

XX 02-MAR-2000.
XX

XX 20-AUG-1999; 99WO-US019021.
XX

XX 21-AUG-1998; 98US-0097457P.
XX

PR 19-AUG-1999; 99US-00377081.
XX

XX (ALBA-) ALBANY MEDICAL COLLEGE.
XX

PA Grasso P, Lee DW, Leinung MC;
XX

XX WPI; 2000-237652/20.
XX

XX Leptin peptides useful for treating pathophysiology relating to
PT homeostasis of body mass such as obesity, anorexia, and hematopoiesis
PT dysfunction and tumor suppression.
XX

PS Claim 26; Fig 16; 121pp; English.
XX

XX The present sequence represents a human leptin. The specification
CC describes peptides derived from leptin. The leptin-derived peptides have
CC increased ability to cross the blood brain barrier and improved bio-
CC availability. Peptides derived from leptin are useful for treating and
CC preventing pathophysiology relating to homeostasis of body mass such as
CC anorexia, obesity comprising hyperglycemia, hyperinsulinemia,
CC hyperphagia, thyroid dysfunction, infertility, type II diabetes mellitus
CC and non-insulin-dependent diabetes mellitus (NIDDM), and hematopoiesis
CC dysfunction and tumor suppression. The peptides are also useful for
CC identifying drugs useful in weight loss diet regimen
XX

SQ Sequence 167 AA;
XX

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVDKTKLTKITVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIFGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLP 120
Db 61 DFIFGLHPILTLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFAKSKCHLP 120
Qy 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSGPC 167
Db 121 WASGLETLDSLGVLGASGYSTEVVALSRLOGLQSLQDMLWQLDLSGPC 167

RESULT 9
AAV80259
ID AAY80259 standard; protein; 167 AA.
XX
AC AAY80259;
XX

DT 25-MAY-2000 (first entry)
XX

DE Human obese OB protein SEQ ID NO:5.
XX

XX Obese; OB protein; polyethylene; polypropylene; weight; obesity;
KW anorectic; gene therapy; type II diabetes mellitus; hypertension;
KW hyperlipidaemia.
XX

OS Homo sapiens.
XX

XX Key Location/Qualifiers
FH Peptide 1..21
FT /label= signal
FT Protein 23..167
FT /label= OB_protein

XX US6025325-A.
XX

XX 15-FEB-2000.
XX

XX 15-MAY-1996; 96US-00648263.
XX

XX 05-MAY-1995; 95US-00435777.
XX

PR 07-JUN-1995; 95US-00484629.
XX

XX (HOFF) HOFFMANN LA ROCHE INC.
XX

XX Guisez Y, Campfield A, Devos R;
XX

XX WPI; 2000-194674/17.
XX

XX N-PSDB; AAZ91516.
XX Polyethylene glycol conjugated proteins useful for modulating the body
PT weight of humans and animals for the prevention, treatment and control of
PT obesity and associated diseases.
XX

PS Disclosure; Col 39-40; 29pp; English.
XX

XX The present invention describes polyethylene glycol conjugated obese (OB)
CC protein compositions (I) useful for modulating the body weight of humans
CC and animals for the prevention, treatment and control of obesity and
CC associated diseases. (I) have anorectic activity and can be used in gene
CC therapy. (I) may be used for the prevention, treatment and control of
CC obesity and associated diseases such as type II diabetes mellitus,
CC hypertension and hyperlipidaemia. The present sequence represents the
CC human OB protein, which can be used in the production of (I)
XX

SQ Sequence 167 AA;
XX

Query Match 100.0%; Score 870; DB 3; Length 167;
XX

QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167

RESULT 12

AAB59914
ID AAB59914 standard; protein; 167 AA.
XX
AC AAB59914;
XX
DT 06-JUN-2001 (first entry)
XX
DE Human leptin fragment SEQ ID NO: 32.
XX
KW Leptin; human; LSR; lipolysis stimulated receptor; obesity; hypertension;
KW anorexia; cachexia; stroke; atherosclerosis.
XX
OS Homo sapiens.
XX
FN WO200121647-A2.
XX
PD 29-MAR-2001.
XX
PF 22-SEP-2000; 2000WO-IB001470.
XX
PR 22-SEP-1999; 99US-0155506P.
XX
PA (GEST) GENSET.
XX
PI Yen F, Erickson MR, Fruebis J, Bihain B;
XX WPI; 2001-218642/22.
XX
PT New leptin polypeptide fragment and related polynucleotides, useful for
PT the prevention and treatment of obesity and obesity-related diseases such
PT as hypertension and diabetes.

PS Claim 1; Page 232-233; 247pp; English.

CC The present invention provides the protein and coding sequences of leptin
CC fragments which modulate the activity of lipolysis stimulated factor
CC (LSR). These sequences are useful in the treatment of obesity related
CC diseases, including obesity, anorexia, cachexia, cardiac and coronary
CC insufficiency, stroke, hypertension, atherosclerotic disease,
CC atherosclerosis, non-insulin dependent diabetes, hyperlipidaemia,
CC hyperuricaemia and syndrome X

SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKV7GL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKV7GL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120

QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167

DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167

RESULT 13

AAB72927
ID AAB72927 standard; protein; 167 AA.
XX
AC AAB72927;
XX
DT 16-MAY-2001 (first entry)
XX
DE Human leptin.
XX
KW Bone resorption modulation; leptin; osteoporosis; Paget's disease;
KW osteoclastogenesis.
XX
OS Homo sapiens.
XX
FN AU200048971-A.
XX
PD 08-FEB-2001.
XX
PF 01-AUG-2000; 2000AU-00048971.
XX
PR 03-AUG-1999; 99AU-00001999.
XX
PA (UYME) UNIV MELBOURNE.
XX
PI Nicholson GC;
XX
DR WPI; 2001-235416/25.
XX
DR N-PSDB; AAF76679.

PT Modulating bone resorption in human or animal for treating osteoporosis
PT or Paget's disease, comprises administering leptin, its derivative,
PT homologue, analog, chemical equivalent, antagonist or agonist.
XX
PS Claim 3; Page 26-27; 40pp; English.
XX
CC The present invention describes a method of modulating bone resorption
CC comprising administering leptin or a derivative under conditions suitable
CC for the modulation of osteoclastogenesis. This is useful in the treatment
CC of osteoporosis and Paget's disease. The present sequence is the human
CC leptin protein sequence
XX
SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKV7GL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAPVQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKV7GL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFAFSKSHLP 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSPGC 167

RESULT 14

AAB10338
ID AAB10338 standard; protein; 167 AA.
XX
AC AAB10338;
XX
DT 10-DEC-2001 (first entry)
XX
DE Human leptin (LEP).
XX
KW Mucosal cell; cell therapy; gene therapy; hyperglycaemia; wound healing;
KW haemophilia; eye damage; diabetes; obesity; degenerative disorder; ulcer;
KW beta-cell destruction; kidney tubule calcification; liver degeneration;

KW diabetic retinopathy; cancer; coronary heart disease; growth disorder;
KW dyslipidaemia; coagulation disorder; stroke; peripheral vascular disease;
KW hypertension; wasting syndrome; passive immunisation; immunosuppressive;
KW Helicobacter pylori; arthritis; cardiovascular disease; ophthalmological;
KW hypoglycaemic; anorectic; coagulant; cerebroprotective; antimicrobial;
KW leptin; LEP; vulnery; cytostatic; hypotensive; cardiatic; human.
XX Homo sapiens.
XX WO200168828-A2.
XX 20-SEP-2001.
XX 12-MAR-2001; 2001WO-IB000722.
XX 13-MAR-2000; 2000US-0188796P.
XX 08-DEC-2000; 2000US-0254464P.
XX (ENGE-) ENGINE INC.
XX Kieffer TJ, Cheung AT;
XX WPI; 2001-582445/65.
XX N-PSDB; AAD17487.
XX Novel isolated or cultured mucosal cell producing nutrient-regulatable
PT protein expressed by transgene comprising expression control element
PT linked with nucleic acid encoding protein, is useful for treating
PT diabetes.
XX Disclosure; Fig 17; 75pp; English.

XX The present invention relates to an isolated or cultured mucosal cell
CC that produces a protein regulatable by a nutrient, where expression of
CC the protein is conferred by a transgene comprising an expression control
CC element in operable linkage with a nucleic acid encoding the protein. The
CC invention is used in cell therapy and gene therapy. Isolated or cultured
CC mucosal cell is useful for treating a hyperglycaemic condition such as
CC type 1 diabetes (insulin-dependent diabetes), where the subject has a
CC fasting plasma glucose level of greater than 110 mg/dl. It is also useful
CC for treating obesity or undesirable body mass. Preferably, in these
CC conditions the mucosal cell expresses insulin, leptin, glucagon-like
CC peptide (GLP)-1, GLP-2, cholecystokinin (CCK), a glucagon antagonist, a
CC growth hormone, a clotting factor or an antibody. The mucosal cells are
CC implanted into a mucosal tissue or non-mucosal tissue such as liver,
CC pancreas or muscle. Mice strains that develop or are susceptible to
CC developing a particular disease (e.g. diabetes, cancer, degenerative
CC disorders etc.) are also useful for introducing therapeutic proteins in
CC order to study the effect of therapeutic protein expression in the
CC disease susceptible mouse. Mucosal cell is also useful for treating
CC insulin-independent (type 2) diabetes, degeneration of pancreas (beta-
CC cell destruction), kidney tubule calcification, degeneration of liver,
CC eye damage (diabetic retinopathy), diabetic foot, ulcerations in mucosa
CC such as mouth and gums, excess bleeding, wound healing or delayed blood
CC coagulation and increased risk of coronary heart disease, stroke,
CC peripheral vascular disease, dyslipidaemia, hypertension and obesity.
CC Mucosal cell also produces protein such as clotting factors to treat
CC haemophilia and other coagulation disorders, growth factors to treat
CC growth disorders or wasting syndrome, and antibodies to provide passive
CC immunisation or protection of a subject against foreign antigens or
CC pathogens e.g. Helicobacter pylori or to provide treatment of cancer,
CC arthritis, or cardiovascular disease. The present sequence is human
XX leptin (LEP)

XX Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGWTLCGFLWLPYLFYQVAPVPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHGWTLCGFLWLPYLFYQVAPVPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

QY 61 DFIGLHPIILTSKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIGLHPIILTSKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLHLVLAFSKSCHLP 120
QY 121 WASGLETUDSLGGVLEASGYSTEVVALSRLOGSLQDMLWQDLSPGC 167
Db 121 WASGLETUDSLGGVLEASGYSTEVVALSRLOGSLQDMLWQDLSPGC 167

RESULT 15
AAU02890

ID AAU02890 standard; protein; 167 AA.

XX AC AAU02890;

XX DT 12-SEP-2001 (first entry)

XX DE Human Ob protein sequence.

XX KW Ob; haematopoietic cytokine; metabolism; weight regulation; inflammation;
KW appetite regulation; mammalian circulatory system; autoimmunity; cancer;
KW immunological response; abnormal proliferation; regeneration; human;
KW degeneration; responsive cell type atrophy.

XX OS Homo sapiens.

XX FH Key Location/Qualifiers

FT Peptide 1..21

FT /note= "Signal peptide"

FT Protein 22..167

FT /note= "Mature human Ob protein"

XX US6225446-B1.

XX PD 01-MAY-2001.

XX PF 05-DEC-1996; 96US-00759628.

XX PR 06-DEC-1995; 95US-0008574P.

XX SCHE) SCHERING CORP.

XX PI Altman SW, Rock FL, Bazan JF, Kastelein RA;

XX WPI; 2001-327467/34.

XX PT Mutational variants of mammalian Ob proteins, useful e.g. for regulating
PT weight and appetite, also in screening or treatment of conditions
PT associated with abnormal proliferation.

XX PS Disclosure; Col 3-4; 24pp; English.

XX CC The sequence represents human Ob protein which belongs to the
CC haematopoietic cytokine subgroup. Cytokines function in regulating
CC metabolism and weight by mediating differentiation and other signals
CC within the mammalian circulatory system. Pure or recombinant mutational
CC variants of mammalian Ob proteins may therefore be used for the
CC regulation of weight and appetite. These mutants and antibodies against
CC them are useful in screening and treatment of conditions associated with
CC abnormal proliferation, such as cancer, and are of use in situations
CC where cytokine functions have been implicated, e.g. immunological
CC responses, inflammation, autoimmunity, regeneration, degeneration and
CC atrophy of responsive cell types

XX SQ Sequence 167 AA;

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 4.8e-85;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGWTLCGFLWLPYLFYQVAPVPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHGWTLCGFLWLPYLFYQVAPVPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

Db 1 MHGTLGFLWLPYLFYVQVPIQKQVDDTKLIKTIIVTRINDISHTSQSVSSKQVTGL 60
Qy 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIIQISNDLENLRDILLHVLAFSKSCHLP 120
Db 61 DFIPGLHPILTLSKMDQTLAVYQQILTSMPSRNVIIQISNDLENLRDILLHVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLQGSLODMLWOLDLSPGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLQGSLODMLWOLDLSPGC 167

Search completed: March 12, 2005, 04:59:47
Job time : 127.85 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:37 ; Search time 120.581 Seconds
(without alignments)
709.207 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWGTLGFLWLPYFYVQ.....SRLLGSLQDMLWQLDLSFGC 167

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt_03.*

1: uniprot_sprot.*

2: uniprot_trembl.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	1	P41159 homo sapien
2	866	99.5	167	1	Q6NT58
3	780	89.7	167	1	OB MACMU
4	733	84.3	146	1	OB PANTR
5	728	83.7	146	1	OB GORGO
6	724	83.2	167	1	OB_FELCA
7	721	82.9	146	1	OB_PONPY
8	715	82.2	167	1	OB_PIG
9	705	81.0	167	1	OB BOVIN
10	704	80.9	167	1	OB_MOUSE
11	690	79.3	167	1	OB_RAT
12	675	77.6	167	1	OB_CANFA
13	640	73.6	163	1	OB_CHICK
14	628	72.2	146	1	OB_T8R8
15	624	71.7	146	1	OB_SHEEP
16	588	67.6	145	2	Q6S9B2
17	576	66.3	145	1	OB_MELGA
18	551	63.3	167	1	OB_SMICR
19	535	61.5	167	2	Q706D0
20	535	61.5	167	2	Q706D1
21	498	57.2	119	2	Q861R2
22	481	55.3	123	2	Q95KW9
23	477	54.8	118	2	Q8MK60
24	476	54.7	118	2	Q8MK58
25	474	54.5	118	2	Q8MK59
26	469	53.9	118	2	Q8MK61
27	449	51.6	109	2	Q866S7
28	447	51.4	99	1	OB_HORSE
29	439	50.5	109	2	Q864V1
30	387	44.5	106	2	Q95MG5
31	380	43.7	90	2	Q8WMK7

RESULT 1

ID	OB_HUMAN	STANDARD;	PRT;	167 AA.
AC	P41159; O15158;			
DT	01-FEB-1995 (Rel. 31, Created)			
DT	01-FEB-1995 (Rel. 31, last sequence update)			
DT	25-OCT-2004 (Rel. 45, last annotation update)			
DE	Leptin precursor (Obesity factor) (Obese protein).			
GN	Name=LEP; Synonyms=OB;			
OS	Homo sapiens (Human).			
OC	Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;			
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.			
OX	NCBI_TaxID=9606;			
RN	SEQUENCE FROM N.A.			
RP	MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;			
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;			
RT	"Positional cloning of the mouse obese gene and its human homologue."			
RL	Nature 372:425-432(1994).			
RN	[2]			
RP	ERRATUM.			
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;			
RL	Nature 374:479-479(1995).			
RN	[3]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=95309556; PubMed=7789654;			
RA	Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,			
RA	Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,			
RA	Nakao K.;			
RT	"Human obese gene expression. Adipocyte-specific expression and			
RL	regional differences in the adipose tissue."			
RL	Diabetes 44:855-858(1995).			
RN	[4]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;			
RA	Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;			
RT	"Genomic structure and promoter analysis of the human obese gene."			
RL	J. Biol. Chem. 271:3971-3974(1996).			
RN	[5]			
RP	SEQUENCE FROM N.A.			
RA	Chehab F.F., Lim M.E.;			
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.			
RN	[6]			
RP	SEQUENCE FROM N.A.			
RA	MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;			
RA	Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,			
RA	Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,			
RA	Nakao K.;			
RT	"Structural organization and chromosomal assignment of the human obese			
RL	gene."			
RL	J. Biol. Chem. 270:27728-27733(1995).			
RN	[7]			
RP	SEQUENCE FROM N.A.			
EX	MEDLINE=96198511; PubMed=8621021;			

32	376	43.2	90	2	Q7TMN2	Q7tmn2 marmota mon
33	375	43.1	90	2	Q7TMN0	Q7tmn0 tamiasciuru
34	371	42.6	91	2	Q7YR78	Q7yr78 bubalus bub
35	368	42.3	90	2	Q8WML2	Q8wml2 oryctolagus
36	367	42.2	90	2	Q8WML1	Q8wml1 chaetophrac
37	367	42.2	90	2	Q7YQJ8	Q7yqj8 vulpes vulp
38	361	41.5	89	2	Q8WML0	Q8wml0 mephitis me
39	361	41.5	89	2	Q6YIR1	Q6yir1 ursus ameri
40	353	40.6	89	2	Q8WMK9	Q8wmk9 procyon lot
41	343.5	39.5	100	2	Q8UWJ3	Q8uwj3 gallus gall
42	342	39.3	90	2	Q8WMK8	Q8wmk8 eptesicus f
43	340	39.1	86	2	Q8MJ10	Q8mj10 bos taurus
44	330	37.9	90	2	Q7TMN1	Q7tmn1 castor cana
45	204	23.4	48	2	Q95MZ8	Q95mz8 bos taurus

RA Niki T., Mori H., Tamori Y., Kishimoto-Hashiramoto M., Ueno H.,
RA Araki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
RA Hashiramoto M., Taniguchi H., Kasuga M.;
RT "Human obese gene: molecular screening in Japanese and Asian Indian
RL NIDDM patients associated with obesity.";
RL Diabetes 45:675-678(1996).
RN [8]
RP SEQUENCE FROM N.A.
RP Lu L., Fu Z., Xu M., Fu Y., Hu Z.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [9]
RP SEQUENCE FROM N.A.
RP TRISUB-Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Datchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Ustin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullaby S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettelman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smalusz D.E.,
RA Schnerch A., Schein J.B., Jones S.J.M., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
RL and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP INTERACTION WITH SIGLEC6.
RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RT "OB-BP1/Siglec-6. A leptin- and sialic acid-binding protein of the
RL immunoglobulin superfamily.";
RL J. Biol. Chem. 274:22729-22738(1999).
RN [11]
RP ERRATUM.
RA Patel N., Brinkman-Van der Linden E.C.M., Altmann S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.;
RL J. Biol. Chem. 274:28058-28058(1999).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
RA Hale J.E.;
RT "Leptin is a four-helix bundle: secondary structure by NMR.";
RL FEBS Lett. 407:239-242(1997).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97289390; PubMed=9144295.
RA Zhang F., Basinski M.B., Beale J.M., Briggs S.L., Churgay L.M.,
RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Hsiung H.M.,
RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.;
RT "Crystal structure of the obese protein leptin-E100.";
RN Nature 387:206-209(1997).
RN [14]
RP VARIANT MET-94.
RA Bartholomew D.W., McClellan J.M.;
RT "A novel polymorphism in the leptin gene.";
RL Hum. Mutat. 12:220-220(1998).
RN [15]
RP VARIANT MORBID OBESITY TRP-105.
RX MEDLINE=98160176; PubMed=9500540;

RA Strobel A., Issa T., Camoin L., Ozata M., Strosberg A.D.;
RT "A leptin missense mutation associated with hypogonadism and morbid
RL Nat. Genet. 18:213-215(1998).
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -1- SUBUNIT: Interacts with SIGLEC6.
CC -1- SUBCELLULAR LOCATION: Secreted.
CC -1- DISEASE: Defects in LEP may be a cause of autosomal recessive
CC obesity [MIM:601665].
CC -1- SIMILARITY: Belongs to the leptin family.
CC -1- DATABASE: NAME=R&D Systems' cytokine mini-reviews: LEP;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=213".
CC -----
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CC -----
CC EMBL; U18915; AAA60470.1; -;
CC EMBL; D49487; BAA08448.1; -;
CC EMBL; U43653; AAC50400.1; -;
CC EMBL; U43415; AAC31660.1; -;
CC EMBL; D63710; BAA09839.1; -;
CC EMBL; D63709; BAA09839.1; JOINED.
CC EMBL; D63518; BAA09787.1; -;
CC EMBL; D63519; BAA09787.1; -;
CC EMBL; AF008123; AAB63507.1; -;
CC EMBL; BC060830; AAH60830.1; -;
CC PIR; A38952; LTHU.
CC PIR; I53166; I53166.
CC PDB; 1AX8; X-ray; @=22-167.
CC Genew; HGNC:6553; LEP.
CC MIM; 164160; -;
CC MIM; 601665; -;
CC GO; GO:0005615; C:extracellular space; TAS.
CC GO; GO:0006112; P:energy reserve metabolism; TAS.
CC InterPro; IPR009079; 4_helix_cytokine.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
CC Polymorphism; Signal.
CC SIGNAL 1 21 Potential.
CC CHAIN 22 167 Leptin.
CC DI-SULFID 117 167
CC VARIANT 49 49 Missing (in 30% the clones).
CC
CC VARIANT 94 94 /FTID=VAR_004196.
CC
CC VARIANT 105 105 V -> M.
CC
CC VARIANT 110 110 R -> W (in morbid obesity and
CC hypogonadism).
CC VARIANT 110 110 /FTID=VAR_008094.
CC
CC CONFLICT 96 96 V -> M (in dbSNP:1800564).
CC HELIX 25 44 /FTID=VAR_011955.
CC HELIX 72 87 Q -> R (in Ref. 8).
CC TURN 88 88
CC TURN 92 114
CC TURN 115 116
CC TURN 128 131
CC HELIX 132 135
CC STRAND 137 137
CC TURN 138 139
CC STRAND 140 140

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FT HELIX 142 160
FT HELIX 161 163

Query Match 100.0%; Score 870; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 8.9e-71;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAVPIQKQVDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAVPIQKQVDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKCHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKCHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOQSLQDMLWQLDLSGPC 167

RESULT 2
Q6NT58 PRELIMINARY; PRT; 167 AA.
AC Q6NT58
DT 05-JUL-2004 (TremBLrel. 27, Created)
DT 05-JUL-2004 (TremBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TremBLrel. 27, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan B., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udell T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smailus D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences.";
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069323; AAH69323.1; -.
DR HSP; P41159; IAX8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR009079; 4 Helix cytokine.
DR InterPro; IPR00065; Leptin.
DR PRINTS; PR00495; Leptin.
DR PRODOM; PD005698; Leptin; 1.
DR SEQUENCE 167 AA; 18612 MW; BE1A046FFB1554DE CRC64;

Query Match 99.5%; Score 866; DB 2; Length 167;
Best Local Similarity 99.4%; Pred. No. 2.1e-70;
Matches 166; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

QY 1 MHWGTLGCGFLWLPYLFVQVAVPIQKQVDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGCGFLWLPYLFVQVAVPIQKQVDDTKTLIKITVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKCHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQLTSMPSRNVQISNDLENLRDLHLVLAFAFSKCHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOQSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOQSLQDMLWQLDLSGPC 167

RESULT 3
OB MACMU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
RA Hosta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
RA Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
monkeys. Effects of insulin, body weight, and non-insulin-dependent
diabetes mellitus.";
RL J. Biol. Chem. 271:25327-25331(1996).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; U58492; AAC50730.1; -.
DR HSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
DR Obesity; Signal.
KW SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
SQ SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BBE9 CRC64;

Query Match 89.7%; Score 780; DB 1; Length 167;
Best Local Similarity 89.8%; Pred. No. 1.3e-62;
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Matches 150; Conservative 10; Mismatches 7; Indels 0; Gaps 0;

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QY 1 MHWCTLCGFLWLPVLFVQAVPIQKQVDDTKTKTIKIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MYWRTLWGLWLPVLFYIQAVPIQKQVDDTKTKTIKIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLKMDQTLAVYQIQLTSMPSRNVQISNDLENRLDLHLVAFSKSCHLP 120
Db 61 DFIPGLHPVLTLSQMDQTLAYQIQLINLPSRNVQISNDLENRLDLHLVAFSKSCHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLSLQDMLWQDLSPGC 167
Db 121 LASGLETLESGLVLEASGYSTEVVALSRLOGLSLQDMLWQDLSPGC 167
```

RESULT 4

```
OB_PANTR
ID OB_PANTR STANDARD; PRT; 146 AA.
AC O02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostock P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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```

```
EMBL; U96450; AB54023.1; -.
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID
SQ SEQUENCE 146 AA; 16058 MW; 02C42A06B554D55C CRC64;
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Query Match 84.3%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.9e-58;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

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QY 22 VPIQVQDDTKTKTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81
Db 1 VPIQVQDDTKTKTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
QY 82 YQIILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 141
```

```
Db 61 YQIILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 120
QY 142 TEVALSRLOGLSLQDMLWQDLSPGC 167
Db 121 TEVALSRLOGLSLQDMLWQDLSPGC 146
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RESULT 5

```
OB_GORGO
ID OB_GORGO STANDARD; PRT; 146 AA.
AC Q95189;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Gorilla gorilla gorilla (lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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```
EMBL; U72872; AB17091.1; -.
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID
SQ SEQUENCE 146 AA; 16031 MW; 02C43BF6B9A4C85C CRC64;
```

Query Match 83.7%; Score 728; DB 1; Length 146;
Best Local Similarity 98.6%; Pred. No. 5.4e-58;
Matches 144; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

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QY 22 VPIQVQDDTKTKTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81
Db 1 VPIQVQDDTKTKTIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
QY 82 YQIILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 141
Db 61 YQIILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDLSGGVLEASGY 120
QY 142 TEVALSRLOGLSLQDMLWQDLSPGC 167
Db 121 TEVALSRLOGLSLQDMLWQDLSPGC 146
```

RESULT 6

```
OB_FELCA
ID OB_FELCA STANDARD; PRT; 167 AA.
```

AC Q9N2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA."
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; AB041360; BAA95481.1; -.
DR HSSP; P41159; 1AX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR ProDom; PD005698; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProBio; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT DIULFID 117 167 By similarity.
SQ SEQUENCE 167 AA; 18583 MW; 643720DBB0AB4B95 CRC64;

Query Match 83.2%; Score 724; DB 1; Length 167;
Best Local Similarity 85.4%; Pred. No. 1.5e-57;
Matches 140; Conservative 12; Mismatches 12; Indels 0; Gaps 0;

Qy 4 GTLCGFLWLPYFYQAVPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFI 63
Db 4 GPLCRFLWLPYLSYVEAPIRKQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFI 63

Qy 64 PGLHPILTSLKMDQTLAVYQIILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWAS 123
Db 64 PGLHPVLSLKMDDTLATYQIILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWAS 123

Qy 124 GLETLDLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167
Db 124 GLETLDLGGVLEASGYSTEVVALSRLOGSLQDMLWQLDLSPGC 167

RESULT 7
OB_PONPY
ID OB_PONPY STANDARD; PRT; 146 AA.
AC Q95234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pongo pygmaeus (Orangutan).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Louis C.F.;

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; U72873; AAB17092.1; -.
DR HSSP; P41159; 1AX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT DIULFID 96 146 By similarity.
SQ SEQUENCE 146 AA; 16195 MW; 3F50A1338FFDBD4 CRC64;

Query Match 82.9%; Score 721; DB 1; Length 146;
Best Local Similarity 97.3%; Pred. No. 2.3e-57;
Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 22 VPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 81
Db 1 VPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSLKMDQTLAV 60

Qy 82 YQIILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLGGVLEASGY 141
Db 61 YQIILTSMPNSRVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDLGGVLEASGY 120

Qy 142 TEVVALSRLOGSLQDMLWQLDLSPGC 167
Db 121 TEVVALSRLOGSLQDMLWQLDLSPGC 146

RESULT 8
OB_PIG
ID OB_PIG STANDARD; PRT; 167 AA.
AC Q23406; O19095; Q95251;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB, OBS;
OS Sus scrofa (Fig).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
OX NCBI_TaxID=9823;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Louis C.F.;

RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE FROM N.A.
 RA Ramsay T.G., Yan X.;
 RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Landrace;
 RA Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G.,
 RA Benkel B.F., McKay R.M., Pelletier G.;
 RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A.
 RA Bidwell C.A., Ji S., Spurlock M.E.;
 RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
 RN [5]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Meishan;
 RA Dai R., Li N., Hu X., Wu C.;
 RL Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE FROM N.A.
 RA McNeel R.L., Mersmann H.J.;
 RT "Adipose tissue regulatory transcript expression in lean versus obese
 RT pigs.";
 RL Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
 RN [7]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Large white;
 RA Soares M.A.M., Euclydes R.F., Guimaraes S.E.F., Martins M.P.,
 RA Lopes P.S.;
 RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
 RN [8]
 RP SEQUENCE OF 15-110 FROM N.A.
 RC TISSUE=White adipose tissue;
 RX MEDLINE=97009821; PubMed=8856925;
 RA Neuenschwander S., Rettenberger G., Meijerink E., Jorg H.,
 RA Stranzinger G.;
 RT "Partial characterization of porcine obesity gene (OBS) and its
 RT localization to chromosome 18 by somatic cell hybrids.";
 RL Anim. Genet. 27:275-278(1996).
 CC -1- FUNCTION: May function as part of a signaling pathway that acts to
 CC regulate the size of the body fat depot. An increase in the level
 CC of LEP may act directly or indirectly on the CNS to inhibit food
 CC intake and/or regulate energy expenditure as part of a homeostatic
 CC mechanism to maintain constancy of the adipose mass.
 CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -1- SIMILARITY: Belongs to the leptin family.
 CC -----
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 CC or send an email to license@sib-sib.ch).
 CC -----
 DR EMBL; U63540; AAB05923.1; -;
 DR EMBL; U59894; AAB03458.1; -;
 DR EMBL; AF026976; AAB82724.1; -;
 DR EMBL; U66254; AAB97308.1; -;
 DR EMBL; AF052691; AAC06303.1; -;
 DR EMBL; AF102856; AAC78147.1; -;
 DR EMBL; AF477387; AAL84792.1; -;
 DR EMBL; AF477386; AAL84792.1; JOINED.
 DR EMBL; U40812; AAC48641.1; -;
 DR HSP; P41159; IAX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR InterPro; IPR000065; Leptin.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPDIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Obesity; Signal.

FT SIGNAL 1 21 Potential.
 FT CHAIN 22 167 Leptin.
 FT DISULFID 117 167 By similarity.
 FT CONFLICT 21 22 AV -> GP (in Ref. 8).
 FT CONFLICT 97 97 I -> L (in Ref. 8).
 FT CONFLICT 122 122 A -> R (in Ref. 4).
 SQ SEQUENCE 167 AA; 18661 MW; 27550E1E0E63814E CRC64;
 Query Match 82.2%; Score 715; DB 1; Length 167;
 Best Local Similarity 85.0%; Pred. No. 9.7e-57;
 Matches 142; Conservative 11; Mismatches 14; Indels 0; Gaps 0;
 Oy 1 MHNGTLCGFLWLPYFYQAVPIQYQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
 Db 1 MRCGFLCRFLWLPYLSYVEAVPIRWYQDDTKTIKTIIVTRISDISHMQSVSSKQKVTGL 60
 Oy 61 DFTPLHPIILTSKMDQTLAVYQIILTSMPSRNVIQISNDLENLRDLHLVAFKSKCHLP 120
 Db 61 DFTPLHPIILTSKMDQTLAVYQIILTSMPSRNVIQISNDLENLRDLHLVAFKSKCHLP 120
 Oy 121 WASGLETLDSIGGVLEASGYSTEVVALSRLOGSLQDMMLWOLDLSPGC 167
 Db 121 QARALETLESIGGVLEASLYSTEVVALSRLOGSLQDMMLWOLDLSPGC 167
 RESULT 9
 OB_BOVIN STANDARD; PRT; 167 AA.
 AC P50595; Q97918; Q95133; Q9TS29;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=LEP; Synonyms=OB, OBS;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OC Bovinae; Bos.
 CX NCBI_TaxID=9913;
 RN [1]
 RP SEQUENCE FROM N.A.
 RC TISSUE=Liver;
 RA Tellam R.L., Briscoe S., Vuocolo A.;
 RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RN [2]
 RP SEQUENCE OF 22-167 FROM N.A.
 RA Ji S., Spurlock M.E.;
 RT "Partial cloning of bovine obesity gene.";
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RN [3]
 RP SEQUENCE OF 22-167 FROM N.A.
 RC TISSUE=White adipose tissue;
 RA Kawakita Y., Abe H., Miyashige T.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RN [4]
 RP SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.
 RC STRAIN=Jersey;
 RX MEDLINE=20063685; PubMed=10594237;
 RA Konfortov B.A., Licence V.E., Miller J.R.;
 RT "Resequencing of DNA from a diverse panel of cattle reveals a high
 RT level of polymorphism in both intron and exon.";
 RL Mamm. Genome 10:1142-1145(1999).
 RN [5]
 RP SEQUENCE FROM N.A., AND VARIANT CYS-25.
 RA Llaferes S.C.;
 RT "genotype effects of bovine leptin mutations on pre- and postpartum
 RT leptin concentrations.";
 RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 46-145 FROM N.A.
 RA Lien S., Sundvold H., Klungland H., Vaage D.I.;
 RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
 RL Anim. Genet. 28:245-245(1997).

```

[7]
RN SEQUENCE OF 60-146 FROM N.A.
RX MEDLINE=96269621; PubMed=8661738;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RL Mamm. Genome 7:398-399(1996).
[8]
RN SEQUENCE OF 1-48 FROM N.A.
RA Fitzsimmons C.J., Schmutz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U43943; AA85906.1; -.
DR EMBL; U50365; AAB61244.1; -.
DR EMBL; U65793; AAB06579.1; -.
DR EMBL; AB003143; AAB019750.1; -.
DR EMBL; AJ132764; CAB64295.1; -.
DR EMBL; AJ236854; CAB38018.1; -.
DR EMBL; AJ512638; CAD54745.1; -.
DR EMBL; AJ512639; CAD54745.1; JOINED.
DR EMBL; Y11369; CAA72197.1; -.
DR EMBL; U43833; AAB18762.1; -.
DR EMBL; AF120500; AAD23567.1; -.
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
DR Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.
FT CONFLICT 25 25 R -> Q (in Ref. 2).
FT CONFLICT 166 166 G -> E (in Ref. 2).
SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 81.0%; Score 705; DB 1; Length 167;
Best Local Similarity 84.4%; Pred. No. 7.8e-56;
Matches 141; Conservative 11; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPVLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MRCGLRFLWLPVLSYVEAPVRKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

QY 61 DFIPLGLPILTSKMDQTLAVYQQILTSMPGRNVQISNDLENRLDLHLVAFKSCPLP 120
DB 61 DFIPLGLPILLSKMDQTLAVYQQILTSMPGRNVQISNDLENRLDLHLVAFKSCPLP 120

QY 121 WASGLETLDSLCGVLEASGYSTEVVALSRQGSLODMLWQDLSPGC 167
DB 121 QVRALESLESGLVLEASLYSTEVVALSRQGSLODMLRQLDLSFGC 167

RESULT 10
OB_MOUSE
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OB_MOUSE STANDARD; PRT; 167 AA.
P41160;
01-FEB-1995 (Rel. 31, Created)
01-FEB-1995 (Rel. 31, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leptin precursor (Obesity factor).
Name=lep; Synonyms=Ob;
Mus musculus (Mouse).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
NCBI_TaxID=10090;
[1]
SEQUENCE FROM N.A.
MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
"Positional cloning of the mouse obese gene and its human homologue.";
Nature 372:425-432(1994).
[2]
ERRATUM.
Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
Nature 374:479-479(1995).
[3]
SEQUENCE FROM N.A.
STRAIN=C57BL/6J;
Chehab F.P., Lim M.B.;
Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
-!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of Lep may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- DISEASE: Defects in Lep are the cause of profound obesity and type
II diabetes.
-!- SIMILARITY: Belongs to the leptin family.

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EMBL; U18812; AAA64564.1; -.
EMBL; U22421; AAA64213.1; -.
PIR; S50863; LTWS.
HSSP; P41159; IAX8.
MGD; MGI:104663; Lep.
GO; GO:0008083; F:growth factor activity; IDA.
GO; GO:0005515; F:protein binding; IPI.
GO; GO:0008206; P:bile acid metabolism; IDA.
GO; GO:0045639; P:positive regulation of myeloid blood cell d. . ; IDA.
GO; GO:0030300; P:regulation of cholesterol absorption; IDA.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR000065; Leptin.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Diabetes mellitus; Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 49 49 Missing (in 30% the clones).
SQ SEQUENCE 167 AA; 18708 MW; D6783B6C76FD7116 CRC64;

Query Match 80.9%; Score 704; DB 1; Length 167;
Best Local Similarity 83.2%; Pred. No. 9.6e-56;
Matches 139; Conservative 13; Mismatches 15; Indels 0; Gaps 0;

QY 1 MHWGTLCGFLWLPVLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MCRPLCRFLWLSYLSYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSAKQRTVL 60

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OY 61 DFIPGLPILTSKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120
DB 61 DFIPGLPILTSKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120

OY 121 WASGLETLDLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
DB 121 QTSGLQKPESLDGVLEASLYSTEVVALSRLOGLQDILQLDVSPEC 167

RESULT 11
OB_RAT OB_RAT STANDARD; PRT; 167 AA.
AC P50596;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=lep; Synonyms=Ob;
OS Rattus norvegicus (Rat).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.
OX NCBI_TaxID=10116;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Testis;
RX MEDLINE=95386724; PubMed=7657834;
RA Ogawa Y., Maizumi H., Isse N., Okazaki T., Mori K., Shigemoto M.,
RA Satoh N., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
RA Nakao K.;
RT "Molecular cloning of rat obese cDNA and augmented gene expression in
RT genetically obese Zucker fatty (fa/fa) rats.";
RL J. Clin. Invest. 96:1647-1652(1995).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Fat;
RX MEDLINE=95314614; PubMed=7794258;
RA Funahashi T., Shimomura I., Hiraoka H., Arai T., Takahashi M.,
RA Nakamura T., Nozaki S., Yamashita S., Takemura K., Tokunaga K.;
RT "Enhanced expression of rat obese (ob) gene in adipose tissues of
RT ventromedial hypothalamus (VMH)-lesioned rats";
RL Biochem. Biophys. Res. Commun. 211:469-475(1995).
RN [3]
RP SEQUENCE FROM N.A.
RC STRAIN=Leto, Oletf, and Zucker; TISSUE=Adipose tissue;
RX MEDLINE=95251725; PubMed=7733988;
RA Murakami T., Shima K.;
RT "Cloning of rat obese cDNA and its expression in obese rats.";
RL Biochem. Biophys. Res. Commun. 209:944-952(1995).
RN [4]
RP SEQUENCE OF 14-167 FROM N.A.
RC STRAIN=Sprague-Dawley; TISSUE=Fat;
RA Donohue P.A., Sivitz W.I., Bailey H.L.;
RL Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of Lep may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
EMBL; D45862; BAA08296.1; -;
EMBL; S78586; AAB34657.2; -;
EMBL; D49653; BAA08529.1; -;

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DR EMBL; U48849; AAC52514.1; -;
DR PIR; PC4034; LTPT.
DR HSP; P41159; IAX8.
DR RGD; 3000; Lep.
DR InterPro; IPR009079; 4 helix_cytokine.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT CONFLICT 32 32 K -> T (in Ref. 2).
FT CONFLICT 163 163 L -> V (in Ref. 4).
SQ SEQUENCE 167 AA; 18866 MW; 3B5B563DA42EC84E CRC64;

Query Match 79.3%; Score 690; DB 1; Length 167;
Best Local Similarity 82.0%; Pred. No. 1.8e-54;
Matches 137; Conservative 13; Mismatches 17; Indels 0; Gaps 0;

OY 1 MHWGTLGGLWLPYLYQVAPVQVPIKVDOTKTLIKTIVTRINDISHTQSVSSKQVTGL 60
DB 1 MCWRPLCRFLWLSYLYQVAPVPIKVDOTKTLIKTIVTRINDISHTQSVSSKQVTGL 60

OY 61 DFIPGLPILTSKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120
DB 61 DFIPGLPILTSKMDOTLAVYQOILTSMPNRNVIQISNDLENLRLDHLHLAFSKSCHLP 120

OY 121 WASGLETLDLGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
DB 121 QTSGLQKPESLDGVLEASLYSTEVVALSRLOGLQDILQLDVSPEC 167

RESULT 12
OB_CANFA OB_CANFA STANDARD; PRT; 167 AA.
AC O02720; Q9TSG1;
DT 15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=lep; Synonyms=OB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Iwase M., Sasaki N., Komagome R., Kimura K., Saito M.;
RT "Molecular cloning of canine leptin cDNA.";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-167 FROM N.A.
RC TISSUE=Adipose tissue;
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of Lep may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----

DR EMBL; AF012727; AAC60368.1; -

DR EMBL; AF082500; AAC32380.1; -

DR HSSP; P41159; IAX8.

DR InterPro; IPR009079; 4 helix_cytokine.

DR InterPro; IPR000065; Leptin.

DR Pfam; PF02024; Leptin.1.

DR PRINTS; PR00495; LEPTIN.

DR ProDom; PD005698; Leptin; 1.

DR Obesity; Signal.

FT SIGNAL 1 18 Potential.

FT CHAIN 19 163 Leptin.

FT DISULFID 113 163 By similarity.

SQ SEQUENCE 163 AA; 18183 MW; 9F578DB2528B18FC CRC64;

Query Match 73.6%; Score 640; DB 1; Length 163;

Best Local Similarity 79.0%; Pred. No. 5.8e-50;

Matches 132; Conservative 13; Mismatches 18; Indels 4; Gaps 2;

QY 1 MHWGTCGFLWLPYLYFVQAVPIQKVQDDTKTLIKTIVTRINDISHTSVSSKQKVTGL 60

Db 1 MCMWRPLCR---LMSVLVYVQAVPCVFQDDTKTLIKTIVTRINDISHT-SVSAKQRVTGL 56

QY 61 DFIPGLHPILTAKMDQTLAVYQOILTSWPNSVIOISNDLENRLDLLHVLAFSKSCHLP 120

Db 57 DFIPGLHPILTSLKMDQTLAVYQOVLTSFQSNVQLIANDLENRLDLLHLLAFSKCSLP 116

QY 121 WASGLQTLDSGLGVLEASYSYEWVALSLQGLSQDMLWQLDLSGPC 167

Db 117 QTSLQKPSLDGLVLEASYSYEWVALSLQGLSQDILQQLDISPEC 163

RESULT 14

Q6T8R8 PRELIMINARY; PRT; 146 AA.

ID O6T8R8 AC O6T8R8; 27, Created)

DT 05-JUL-2004 (T-EMBLrel. 27, Last sequence update)

DT 05-JUL-2004 (T-EMBLrel. 27, Last annotation update)

DE Leptin (Fragment).

OS Bubalus bubalis (Domestic water buffalo).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae; Bovinae; Bubalus.

OC NCBI_TaxID=89462;

RN [1]

RN SEQUENCE FROM N.A.

RP TISSUE=Adipose tissue;

RC Rajendran S., Shukla D.C., Saravanan B.C.;

RL Submitted (Oct-2003) to the EMBL/GenBank/DBJ databases.

DR EMBL; AY427959; AAR05862.1; -

DR HSSP; P41159; IAX8.

DR GO; GO:0005576; C:extracellular; IEA.

DR GO; GO:0003179; F:hormone activity; IEA.

DR GO; GO:0007165; P:signal transduction; IEA.

DR InterPro; IPR009079; 4 helix_cytokine.

DR InterPro; IPR000065; Leptin.

DR Pfam; PF02024; Leptin.1.

DR PRINTS; PR00495; LEPTIN.

DR ProDom; PD005698; Leptin; 1.

DR NON_TER 1 1

FT CHAIN <1 146 leptin.

SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 72.2%; Score 628; DB 2; Length 146;

Best Local Similarity 87.0%; Pred. No. 6.1e-49;

Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

```
Qy 22 VPIQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Db 1 VPIRKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAI 60
Qy 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
Db 61 YQQLTSLPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 142 TEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 TEVVALSRLOGLQDMLRQLDLSFGC 146

RESULT 15
OB SHEEP
ID OB SHEEP STANDARD; PRT; 146 AA.
AC Q28603; P79212;
DT 01-NOV-1997 (Rel. 35, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Ovis aries (Sheep).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Caprinae; Ovis.
OC NCBI_TaxID=9940;
RN (1)
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Simmons J.M., Dyer C.J., Keisler D.H.;
RL Submitted (JAN-1997) to the EMBL/GenBank/DBJ databases.
RP (2)
RP SEQUENCE OF 9-125 FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=98006799; PubMed=9347250; DOI=10.1016/S0739-7240(97)00028-3;
RA Dyer C.J., Simmons J.M., Matteri R.L., Keisler D.H.;
RT "cDNA cloning and tissue-specific gene expression of ovine leptin,
RL NPY-Y1 receptor, and NPY-Y2 receptor."
RL Domest. Anim. Endocrinol. 14:295-303(1997).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC -----
CC This SWISS-PROT entry is copyright. It is produced through a collaboration
CC between the Swiss Institute of Bioinformatics and the EMBL outstation -
CC the European Bioinformatics Institute. There are no restrictions on its
CC use by non-profit institutions as long as its content is in no way
CC modified and this statement is not removed. Usage by and for commercial
CC entities requires a license agreement (See http://www.isb-sib.ch/announce/
CC or send an email to license@isb-sib.ch).
CC -----
DR EMBL; U84247; AAB41786.1; -.
DR EMBL; U62123; AAB51033.1; -.
DR HSPSP; P41159; IAX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
FT CONFLICT 65 65 L -> H (in Ref. 2).
FT CONFLICT 92 92 A -> G (in Ref. 2).
FT CONFLICT 124 124 V -> L (in Ref. 2).
SQ SEQUENCE 146 AA; 16053 MW; 19DS4C53240968CA CRC64;

Query Match 71.7%; Score 624; DB 1; Length 146;
Best Local Similarity 87.0%; Pred. No. 1.4e-48;
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Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
Qy 22 VPIQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
Db 1 VPIRKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAI 60
Qy 82 YQQLTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141
Db 61 YQQLTSLPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 142 TEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 TEVVALSRLOGLQDMLRQLDLSFGC 146

Search completed: March 12, 2005, 05:03:38
Job time : 122.581 secs
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:03 ; Search time 109.15 Seconds
(without alignments)
517.333 Million cell updates/sec

Title: US-10-049-182-6

Perfect score: 736

Sequence: 1 VPIQKVQDPTLTKITVTR.....SRLOGLQDMLWQLDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : A_Geneseq_16Dec04.*

- 1: Geneseqp1980s.*
- 2: Geneseqp1990s.*
- 3: Geneseqp2000s.*
- 4: Geneseqp2001s.*
- 5: Geneseqp2002s.*
- 6: Geneseqp2003as.*
- 7: Geneseqp2003bs.*
- 8: Geneseqp2004s.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	146	2 AAW00013	Acid stab
2	736	100.0	146	2 AAR99490	Chimeric
3	736	100.0	146	2 AAW00539	Human mat
4	736	100.0	146	2 AAW30892	Synthetic
5	736	100.0	146	2 AAW34482	Human obe
6	736	100.0	146	2 AAW10151	Properly
7	736	100.0	146	2 AAW22901	Biologica
8	736	100.0	146	2 AAW30791	Obesity p
9	736	100.0	146	2 AAW26194	Obesity p
10	736	100.0	146	2 AAW34483	Human obe
11	736	100.0	146	2 AAW32575	Anti obes
12	736	100.0	146	2 AAW34489	Obesity p
13	736	100.0	146	2 AAW69682	Human obe
14	736	100.0	146	2 AAW53342	Obesity p
15	736	100.0	146	2 AAY43311	Human lep
16	736	100.0	146	2 AAY06102	Human obe
17	736	100.0	146	3 AAY92712	Mature le
18	736	100.0	146	3 AAY82111	Mature hu
19	736	100.0	146	3 AAY80260	Human mat
20	736	100.0	146	3 AAY83768	Human OB
21	736	100.0	146	3 AAY97871	Mature wi
22	736	100.0	146	3 AAY95786	Mature re
23	736	100.0	146	3 AAY95531	Human mat
24	736	100.0	146	3 AAB14265	Mature hu
25	736	100.0	146	4 AAB70130	Mature hu

26	736	100.0	146	5 AAE23614	Human lep
27	736	100.0	146	5 ABG32264	Recombina
28	736	100.0	146	5 ABP63579	Human obe
29	736	100.0	146	5 ADG65529	Human lep
30	736	100.0	146	6 ABR57162	Recombina
31	736	100.0	146	7 ADC06694	Leptin ta
32	736	100.0	146	7 ADD26675	Human adi
33	736	100.0	146	7 ADD71107	Human lep
34	736	100.0	146	8 ADL80474	Mature hu
35	736	100.0	146	8 ADL88877	Human cyt
36	736	100.0	147	2 AAW34394	Human Met
37	736	100.0	147	2 AAW27167	Human rsc
38	736	100.0	147	2 AAW53328	Human obe
39	736	100.0	147	2 AAY43314	Human lep
40	736	100.0	147	3 AAY92261	Mature re
41	736	100.0	148	2 AAW07192	Human ant
42	736	100.0	148	2 AAW28801	Human mas
43	736	100.0	148	2 AAW71849	Obesity p
44	736	100.0	166	2 AAW00535	Human obe
45	736	100.0	167	2 AAW03694	Human obe

ALIGNMENTS

RESULT 1

AAW00013
ID AAW00013 standard; protein; 146 AA.
XX
AC AAW00013;
XX
DT 30-SEP-1996 (first entry)
XX
DE Acid stable modified ob protein (Asp22Asn).
XX
KW ob protein; adiposity regulating hormone; mouse; acid stability;
KW adsorption characteristic; obesity; type II diabetes;
KW cardiovascular disease; cancer.
XX
OS Synthetic.
XX
FH Key Location/Qualifiers
FT Misc-difference 22 /label= Asp22Asn
FT Disulfide-bond 96. .146
XX
PN EP725078-Al.
XX
PD 07-AUG-1996.
XX
PF 29-JAN-1996; 96EP-00300612.
XX
PR 31-JAN-1995; 95US-00381048.
PR 06-FEB-1995; 95US-00383638.
XX
(ELIL) LILLY & CO ELI.
XX
PI Basinsky MB, Dimarchi RD, Heath WF, Schoner BE;
XX
DR WPI; 1996-356062/36.
XX

Mammalian derived anti-obesity proteins which regulate fat tissue - used for treating obesity and to reduce risk for type II diabetes, cardiovascular disease and cancer.

Example 4; Page 19; 42pp; English.

This sequence represents a modified ob proteins. ob proteins are thought to be adiposity regulating hormones. This sequence is based on the mouse ob protein sequence. Proteins such as this have improved stability, esp. acid stability, and improved adsorption characteristics compared to the wild type protein disclosed in Yiyang Zhang et al, Nature 372: 425-32 (December 1994). These proteins correspond to the generic formulae given

CC in AAR99497-98). They are biologically active for the treatment of
 CC obesity. Individuals treated with these proteins have a reduced risk for
 CC type II diabetes, cardiovascular disease and cancer
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
 DB 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQOILTSMPERNVQISNDLENRLDLHLVLAFLAFSKSCHLPWASGLTDLSDLGVLASGYS 120
 DB 61 YQOILTSMPERNVQISNDLENRLDLHLVLAFLAFSKSCHLPWASGLTDLSDLGVLASGYS 120

QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
 DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 2
 AAR99490
 ID AAR99490 standard; protein; 146 AA.
 XX
 AC AAR99490;
 XX
 DT 16-OCT-2003 (revised)
 DT 26-SEP-1996 (first entry)
 XX
 DE Chimeric ob protein.
 XX
 KW ob protein; human; substitution; murine; mouse; obesity; stability;
 KW type II diabetes; cardiovascular disease; cancer.
 XX
 OS Mus musculus.
 OS Homo sapiens.
 OS Chimeric.

PH Key Location/Qualifiers
 FT Misc-difference 22 /note= "Opt. Gln or Asp"
 FT Misc-difference 27 /note= "Opt. Ala"
 FT Misc-difference 28 /note= "Opt. Glu or absent"
 FT Misc-difference 54 /note= "Opt. Ala"
 FT Misc-difference 68 /note= "Opt. Leu"
 FT Misc-difference 72 /note= "Opt. Glu or Asp"
 FT Misc-difference 77 /note= "Opt. Ala"
 FT Disulfide-bond 96.146
 FT Misc-difference 97 /note= "Opt. replaced with Gln, Asn, Ala, Gly, Ser or Pro"
 FT Misc-difference 100 /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
 FT Misc-difference 101 /note= "Opt. replaced with Ser, Asn, Gly, His, Pro, Thr or Val"
 FT Misc-difference 102 /note= "Opt. replaced with Arg"
 FT Misc-difference 103 /note= "Opt. replaced with Ala"
 FT Misc-difference 105 /note= "Opt. replaced with Gln"
 FT Misc-difference 106

FT Misc-difference 107 /note= "Opt. replaced with Lys or Ser"
 FT Misc-difference 108 /note= "Opt. replaced with Pro"
 FT Misc-difference 111 /note= "Opt. replaced with Glu"
 FT Misc-difference 118 /note= "Opt. replaced with Asp"
 FT Misc-difference 138 /note= "Opt. Leu"
 FT /note= "Opt. replaced with Ala, Glu, Asp, Asn, Met, Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
 XX
 PN EP725079-A1.
 PD 07-AUG-1996.
 XX 29-JAN-1996; 96EP-00300613.
 PR 31-JAN-1995; 95US-00381048.
 PR 06-FEB-1995; 95US-00383638.
 PR 22-JUN-1995; 95US-0000450P.
 PR 11-AUG-1995; 95US-0002161P.
 XX
 PA (ELIL) LILLY & CO ELI.
 XX
 PI Basinski MB, Dimarchi RD, Flora DB, Hale JE, Heath WF;
 PI Hoffmann JA, Schoner BE;
 XX
 DR WPI; 1996-356063/36.
 DR N-PSDB; AAT34254.
 XX
 PT Modified human anti-obesity proteins which regulate fat tissue - have
 PT increased stability, for treating obesity and to reduce risk for type II
 PT diabetes, cardiovascular disease and cancer.
 XX
 PS Claim 3; Page 47; 56pp; English.
 XX
 CC The sequences given in AAR99490-96 represent modified ob proteins which
 CC are based on the human ob protein sequence. These protein sequences are
 CC covered by the generic sequence given in AAR99489. In these proteins,
 CC specific amino acids are substituted for the residues found in the
 CC corresponding positions in murine ob protein. These proteins are
 CC biologically active for the treatment of obesity, and are more stable
 CC than either the murine or human proteins. Individuals treated with these
 CC proteins have a reduced risk for type II diabetes, cardiovascular disease
 CC and cancer. (Updated on 16-OCT-2003 to standardise OS field)
 XX
 SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
 DB 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60

QY 61 YQOILTSMPERNVQISNDLENRLDLHLVLAFLAFSKSCHLPWASGLTDLSDLGVLASGYS 120
 DB 61 YQOILTSMPERNVQISNDLENRLDLHLVLAFLAFSKSCHLPWASGLTDLSDLGVLASGYS 120

QY 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146
 DB 121 TEVVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 3
 AAR99490
 ID AAR99490 standard; protein; 146 AA.
 XX
 AC AAR99490;
 XX

```
DT 13-SEP-1996 (first entry)
XX Human mature obesity protein.
DE
XX
XX Obesity; mouse; OBP; leptin; hormone; body weight regulation; diabetes;
KW food intake; energy expenditure; high blood pressure; cholesterol; human;
KW gene therapy; antibody; cancer; Kobe beef; Foie gras; immunoassay.
XX
XX Homo sapiens.
OS
XX GB2292382-A.
PN
XX
XX 21-FEB-1996.
PD
XX
XX 17-AUG-1995; 95GB-00016947.
PF
XX
XX 17-AUG-1994; 94US-00292345.
PR
XX 30-NOV-1994; 94US-00347563.
PR
XX 10-MAY-1995; 95US-00438431.
PR
XX 07-JUN-1995; 95US-00483211.
XX
XX (UVRQ) UNIV ROCKEFELLER.
PA
XX
XX Friedman JM, Zhang Y, Proenca R, Maffei M, Halaas JL, Gajiwala K;
PI Burley SK;
PI
XX
XX WPI; 1996-099009/11.
DR
XX
XX Obesity polypeptide(s) able to modulate body wt. - useful for e.g.
PT reducing wt. in treatment of diabetes, high blood pressure and high
PT cholesterol and for cosmetic reasons.
PT
XX
XX Claim 11; Page ?; 304pp; English.
PS
XX
XX AAW00538-W00541 represent the mature proteins of the murine and human
CC obesity polypeptides (OBP) (full length sequences represented by AAR92719
CC and AAR92720). OBP (also known as leptin) is a hormone involved in the
CC regulation of body weight. This sequence has effects on both food intake
CC and energy expenditure. OBP and its analogues are useful for modifying
CC body weight (optionally combined with known medicaments), for treating
CC diabetes, high blood pressure or high cholesterol. The DNA encoding this
CC sequence (and sequences complementary to it) can be used in gene therapy
CC for modifying body weight. This protein can be used for reducing weight
CC for health or cosmetic reasons in obese humans, or to produce leaner food
CC animals. Antagonists of OBP (including antibodies) are useful for
CC increasing body weight, e.g. for treating weight loss associated with
CC cancer, or for cosmetic reasons in humans, or for production of Kobe beef
CC or Foie gras in domestic animals. OBP antibodies (Ab) can also be used in
CC diagnostic immunoassays for the presence of OBP. The formation of Ab-OBP
CC complexes enables in vitro evaluation of levels of OBP in a sample,
CC especially to detect diseases associated with elevated or decreased
CC levels, and to monitor treatment of these diseases
XX
XX Sequence 146 AA;
SQ
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQVGTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSMPSNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYS 120
DB 61 YQOILTSMPSNRNVIQISNDLENLRDLHLVAFSKSCHLPWASGLTLDLSLGGVLEASGYS 120
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
RESULT 5
AAW34482
ID AAW34482 standard; protein; 146 AA.
XX
XX AAW34482;
AC
XX 17-MAR-1998 (first entry)
DT
XX Human obesity protein.
DE
XX Obesity protein; therapy; obesity associated disorder; human.
KW
XX Homo sapiens.
OS
```

RESULT 4

PN EP784979-A2.
 XX 23-JUL-1997.
 PD 17-JAN-1997; 97EP-00300299.
 PF 19-JAN-1996; 96US-0010229P.
 XX 07-FEB-1996; 96GB-00002408.
 XX (ELIL) LILLY & CO ELI.
 XX Beals JM, Dodd SW, Pekar AH;
 XX WPI; 1997-365736/34.
 DR New obesity protein compositions - comprising a soluble parenteral
 PT formulation containing a preservative selected from an alkyl:paraben and
 PT chlorobutanol.
 XX Disclosure; Page 6; 15pp; English.
 XX This sequence represents the human obesity protein. It can be used in the
 CC formulation of the invention. The formulation of the invention is a
 CC soluble parenteral formulation that comprises an obesity protein and a
 CC preservative selected from an alkylparaben, chlorobutanol, or a mixture.
 CC The compositions can be used for treating obesity and disorders
 CC associated with obesity. In the formulations, the obesity protein remains
 CC stable and soluble at much higher concentrations and at a pH range
 CC acceptable for a soluble, parenteral formulation
 XX Sequence 146 AA;
 SQ
 Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 QY 121 TEVALSRLOGLQDMLWQLDLSFGC 146
 Db 121 TEVALSRLOGLQDMLWQLDLSFGC 146
 RESULT 6
 AAW10151
 ID AAW10151 standard; protein; 146 AA.
 XX AAW10151;
 AC 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Properly folded obesity protein intermediate.
 DE Intermediate; recombinant; production; obesity; regulation; fatty tissue;
 XX treatment; disease; diabetes; cardiovascular; cancer; properly folded.
 KW Mammalia.
 XX Key Location/Qualifiers
 XX Modified-site 1
 FT /label= Val-R3
 FT /note= "R3 is absent, Met, Met-R4 or leader sequence
 FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
 FT and R4 is any amino acid other than Pro"
 FT Modified-site 96
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys146 is
 FT free Cys residue"
 FT Modified-site 146
 FT /note= "free Cys residue or part of mixed disulfide with,
 FT e.g. Cys, glutathione or 2-mercaptoethanol when Cys96 is
 FT free Cys residue"
 PN W09700886-A1.
 XX 09-JAN-1997.
 PD 20-JUN-1996; 96WO-US010613.
 XX 22-JUN-1995; 95US-0000451P.
 XX (ELIL) LILLY & CO ELI.
 XX Hale JE, Mackellar W;
 XX WPI; 1997-087317/08.
 DR Properly folded intermediate for obesity protein - prepd. from inclusion
 PT bodies, provides high yield of active protein for treatment of obesity
 PT and its complications.
 XX Claim 1; Page 21; 66pp; English.
 CC AAW10151 is a properly folded intermediate for the production of the
 CC biologically active obesity protein AAW22901, which has a similar
 CC structure but comprises a disulphide bridge between Cys96 and Cys146.
 CC AAW10151 is the final intermediate in the renaturation of a recombinant
 CC protein to AAW22901, which is an active anti-obesity protein for the
 CC regulation of fatty tissue and treatment of obesity related diseases,
 CC e.g. diabetes, cardiovascular disease and cancer. The production of
 CC AAW22901 via AAW10151 provides a high yield of active protein, and
 CC permits large scale manufacture with a high concentration of protein
 CC during the folding stage. AAW10151 already has the correct tertiary
 CC structure and conversion to AAW22901 is almost quantitative, with minimal
 CC formation of S-S linked dimers or multimers, negating the need for an
 CC aggregation preventing agent. AAW10151 is stable in the presence or
 CC absence of denaturant, is soluble in phosphate buffered saline and can be
 CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
 XX Sequence 146 AA;
 SQ
 Query Match 100.0%; Score 736; DB 2; Length 146;
 Best Local Similarity 100.0%; Pred. No. 7.8e-73;
 Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLKMDQTLAV 60
 Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKOKVTGLDFIPGLHPILTLKMDQTLAV 60
 QY 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 Db 61 YQOILTSMPSNRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
 QY 121 TEVALSRLOGLQDMLWQLDLSFGC 146
 Db 121 TEVALSRLOGLQDMLWQLDLSFGC 146
 RESULT 7
 AAW22901
 ID AAW22901 standard; protein; 146 AA.
 XX AAW22901;
 AC 27-AUG-2003 (revised)
 DT 02-OCT-1997 (first entry)
 XX Biologically active obesity protein.
 DE

KW Intermediate; recombinant; production; obesity; regulation; fatty tissue;
XX treatment; disease; diabetes; cardiovascular; cancer; properly folded.
XX Mammalia.

XX Key Location/Qualifiers
XX Modified-site 1
XX /label= Val-R3

FT /note= "R3 is absent, Met, Met-R4 or leader sequence
FT (preferably Met-Arg, Gly-Ser-Pro or 1 of AAW08589-94),
FT and R4 is any amino acid other than Pro"
FT Disulfide-bond 96. 146

XX
XX WO9700886-A1.

XX
XX 09-JAN-1997.

XX
XX 20-JUN-1996; 96WO-US010613.

XX
XX 22-JUN-1995; 95US-0000451P.

XX
XX (ELIL) LILLY & CO ELI.

XX
XX Hale JE, Mackellar W;

XX
XX WPI; 1997-087317/08.

XX Properly folded intermediate for obesity protein - prepd. from inclusion
PT bodies, provides high yield of active protein for treatment of obesity
PT and its complications.

XX
XX Claim 12; Page 21; 66pp; English.

XX AAW10151 is a properly folded intermediate for the production of the
CC biologically active obesity protein AAW22901, which has a similar
CC structure but comprises a disulfide bridge between Cys96 and Cys146.
CC AAW10151 is the final intermediate in the renaturation of a recombinant
CC protein to AAW22901, which is an active anti-obesity protein for the
CC regulation of fatty tissue and treatment of obesity related diseases,
CC e.g. diabetes, cardiovascular disease and cancer. The production of
CC AAW22901 via AAW10151 provides a high yield of active protein, and
CC permits large scale manufacture with a high concentration of protein
CC during the folding stage. AAW10151 already has the correct tertiary
CC structure and conversion to AAW22901 is almost quantitative, with minimal
CC formation of S-S linked dimers or multimers, negating the need for an
CC aggregation preventing agent. AAW10151 is stable in the presence or
CC absence of denaturant, is soluble in phosphate buffered saline and can be
CC purified and characterised. (Updated on 27-AUG-2003 to correct OS field.)
XX

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 61 YQOILTSMPSPNRVQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPSPNRVQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

Qy 121 TEVALSRLOGLSQDMLWQLDLSFGC 146

Db 121 TEVALSRLOGLSQDMLWQLDLSFGC 146

RESULT 8

AAW30791

ID AAW30791 standard; protein; 146 AA.

XX
XX
AC AAW30791;

XX
DT

12-MAR-1998 (first entry)

Obesity protein complexed with a divalent metal cation.

XX
DE
XX
XX Obesity protein; diabetes; cancer; cardiovascular disease;
KW divalent metal cation; leader sequence.
XX

OS Homo sapiens.

XX Key Location/Qualifiers

FT Disulfide-bond 96. 146

XX
XX WO9728824-A1.

XX
XX 14-AUG-1997.

XX
XX 24-JAN-1997; 97WO-US001188.

XX
XX 06-FEB-1996; 96US-0011238P.

XX
XX (ELIL) LILLY & CO ELI.

XX
XX Hoffmann JA;

XX
XX WPI; 1997-415077/38.

XX New compound comprising obesity protein and divalent metal cation - for
PT treatment of obesity and associated conditions, required at lower dose
PT than free protein.

XX
XX Claim 3; Page 26; 33pp; English.

XX The present sequence represents a human obesity protein, which is
CC complexed with a divalent metal cation e.g. zinc and optionally has a
CC leader sequence. It is used to treat obesity and conditions (particularly
CC type II diabetes, cardiovascular disease and cancer) associated with it.
CC When formulated with the metal ion, it is more active, allowing reduction
CC in dose and thus reduction in cost and toxic side effects
XX

SQ Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Qy 61 YQOILTSMPSPNRVQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQOILTSMPSPNRVQISNDLENLRDLHLVLAFAKSKCHLPWASGLETLDSLGGLVLEASGYS 120

Qy 121 TEVALSRLOGLSQDMLWQLDLSFGC 146

Db 121 TEVALSRLOGLSQDMLWQLDLSFGC 146

RESULT 9

AAW26194

ID AAW26194 standard; protein; 146 AA.

XX
XX AAW26194;

DT 18-FEB-1998 (first entry)

DE Obesity protein analogue #6.

XX Obesity protein analogue; divalent metal cation complex; therapy; cancer;
KW obesity; obesity associated disorder; diabetes; cardiovascular disease.

OS Synthetic.

XX FH Key Location/Qualifiers
FT Disulfide-bond 96. .146
FT Misc-difference 97
FT /note= "optionally replaced with Gln, Asn, Ala, Gly, Ser
or Pro"
FT Misc-difference 100
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
FT Misc-difference 101
FT /note= "optionally replaced with Ser, Asn, Gly, His, Pro,
Thr or Val"
FT Misc-difference 102
FT /note= "optionally replaced with Arg"
FT Misc-difference 103
FT /note= "optionally replaced with Ala"
FT Misc-difference 105
FT /note= "optionally replaced with Gln"
FT Misc-difference 106
FT /note= "optionally replaced with Lys or Ser"
FT Misc-difference 107
FT /note= "optionally replaced with Pro"
FT Misc-difference 108
FT /note= "optionally replaced with Glu"
FT Misc-difference 111
FT /note= "optionally replaced with Asp"
FT Misc-difference 138
FT /note= "optionally replaced with Ala, Glu, Asp, Asn, Met,
Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val or Leu"
XX WO9726916-A1.
XX 31-JUL-1997.
XX 24-JAN-1997; 97WO-US001189.
XX 25-JAN-1996; 96US-0011055P.
XX (ELIL) LILLY & CO ELI.
XX Hoffmann JA;
XX WPI; 1997-393377/36.
XX Obesity protein analogue complexed with divalent metal cation - useful
for treating obesity and associated disorders, e.g. diabetes,
cardiovascular disease and cancer.
XX Disclosure; Page 11; 45pp; English.
XX AAW26199, AAW26190 and AAW26192-W26201 represent obesity protein
analogues contained in the compound of the invention. These sequences
were synthetically created from the sequence shown in AAW26191. The
compound of the invention comprises one of these obesity protein
analogues complexed with a divalent metal cation (preferably Zn⁺⁺). The
specification does not indicate where the divalent metal cation complexes
to on the obesity protein analogue. The compound of the invention (or a
parenteral pharmaceutical formulation containing it) can be used to treat
obesity. It may also be used to treat disorders associated with obesity
such as diabetes, cardiovascular disease and cancer. The compound allows
effective pharmacological treatment at lower doses than significantly
reduce the risk of toxic or other undesirable effects. In addition,
because the amount of protein administered is less, the cost of the unit
dosage form to the patient is reduced
XX Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
|||||

Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
QY 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
|||||
Db 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
|||||
QY 121 TEVALSRLQGSLOQDMLWQLDLSFGC 146
|||||
Db 121 TEVALSRLQGSLOQDMLWQLDLSFGC 146
|||||
RESULT 10
AAW34483
ID AAW34483 standard; protein; 146 AA.
XX AC AAW34483;
XX 17-MAR-1998 (first entry)
DE Human obesity protein.
XX Obesity protein; therapy; obesity associated disorder; human.
XX Homo sapiens.
XX EP784981-A2.
XX 23-JUL-1997.
XX 17-JAN-1997; 97EP-00300300.
XX 19-JAN-1996; 96US-0010357P.
XX 07-FEB-1996; 96GB-00002410.
XX (ELIL) LILLY & CO ELI.
XX Beals JM, Dodd SW, Millican RL, Pekar AH;
XX WPI; 1997-365737/34.
XX New obesity protein compositions - comprising a soluble parenteral
formulation containing a preservative and having low ionic strength.
XX Disclosure; Page 7; 17pp; English.
XX This sequence represents the human obesity protein. It can be used in the
formulation of the invention. The formulation of the invention is a
soluble parenteral formulation that comprises an obesity protein and a
preservative, the formulation having an ionic strength of less than about
10 mM. The compositions can be used for treating obesity and disorders
associated with obesity. In the formulations the obesity protein remains
soluble at much higher concentration and at the desired pH range
XX Sequence 146 AA;
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 7.8e-73;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
|||||
Db 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLISKMDQTLAV 60
|||||
QY 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
|||||
Db 61 YQOILTSMPERNVIOISNDLENLRLDLHLVLAFAFSKCHLPWASGLETLDSLGVLASGYS 120
|||||
QY 121 TEVALSRLQGSLOQDMLWQLDLSFGC 146
|||||
Db 121 TEVALSRLQGSLOQDMLWQLDLSFGC 146
|||||
RESULT 11

CC and a preservative selected from an alkylparaben, chlorobutanol, or a
CC mixture. The compositions can be used for the treatment of obesity and
CC disorders associated with obesity. In the formulations, the obesity
CC protein analogue remains stable and soluble at much higher concentrations
CC and at a pH range acceptable for a soluble, multi-use parenteral
CC formulation

XX Sequence 146 AA;

SQ Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73; Indels 0; Gaps 0;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120

QY 121 TEWVALSRLOGLQDMLWQLDLSGPC 146

Db 121 TEWVALSRLOGLQDMLWQLDLSGPC 146

RESULT 13

AAW69682

ID AAW69682 standard; protein; 146 AA.

XX AC AAW69682;

XX DT 07-DEC-1998 (first entry)

XX DE Human obesity protein.

XX KW Obesity protein; therapy; human.

XX OS Homo sapiens.

XX PN WO9831391-A1.

XX PD 23-JUL-1998.

XX PF 16-JAN-1998; 98WO-US000939.

XX PR 17-JAN-1997; 97US-0035714P.

XX PR 07-AUG-1997; 97US-0054886P.

XX PA (ELIL) LILLY & CO ELI.

XX PI Rinella JV;

XX WPI; 1998-413818/35.

XX Obesity protein, soluble formulation for treating obesity - has pH greater

XX than 8.0, at which aggregation of obesity proteins by preservatives is

XX reduced allowing production of multi-use formulation.

XX Disclosure; Page 11-12; 30pp; English.

XX This is the amino acid sequence of human obesity protein. The invention
XX discloses a storage-stable, soluble formulation comprising an obesity
XX protein and a preservative, and having a pH greater than 8.0. The obesity
XX protein used in the formulation is preferably bio-synthesized in a host
XX cell transformed with a recombinant DNA comprising a synthetic or semi-
XX synthetic DNA encoding tge protein. The soluble formulation can be
XX administered to mammals to treat obesity (claimed), especially humans
XX when the obesity protein is human obesity protein. It was found that the
XX physical stability of obesity proteins in the presence of preservatives
XX such as phenol and cresol changes abruptly and is greatly enhanced at pH
XX values above 8.0, such that the aggregation of obesity proteins caused by
XX preservatives is reduced. At pH above 8.0, obesity proteins remain in

CC solution in the presence of certain preservatives, making possible a
CC multi-use parenteral formulation containing those preservatives

XX Sequence 146 AA;

Query Match 100.0%; Score 736; DB 2; Length 146;

Best Local Similarity 100.0%; Pred. No. 7.8e-73;

Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

Db 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120

Db 61 YQOILTSMPNRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120

QY 121 TEWVALSRLOGLQDMLWQLDLSGPC 146

Db 121 TEWVALSRLOGLQDMLWQLDLSGPC 146

RESULT 14

AAW53342

ID AAW53342 standard; protein; 146 AA.

XX AC AAW53342;

XX DT 20-JUL-1998 (first entry)

XX DE Obesity protein analogue formula II SEQ ID NO:4.

XX KW Human; obesity protein; soluble; parenteral formulation; anionic;

XX KW amphiphilic; ob gene; Ob protein.

XX OS Synthetic.

XX Key Location/Qualifiers

XX FH Misc-difference 97

XX FT /note= "His can be replaced with Gln, Asn, Ala, Gly, Ser,

XX or Pro"

XX FT Misc-difference 100

XX FT /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met,

XX Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu"

XX FT Misc-difference 101

XX FT /note= "Ala can be replaced with Ser, Asn, Gly, His, Pro,

XX Thr, Val"

XX FT /note= "Ser can be replaced with Arg"

XX FT Misc-difference 103

XX FT /note= "Gly can be replaced with Ala"

XX FT Misc-difference 105

XX FT /note= "Glu can be replaced with Gln"

XX FT Misc-difference 106

XX FT /note= "Thr can be replaced with Lys or Ser"

XX FT Misc-difference 107

XX FT /note= "Leu can be replaced with Pro"

XX FT Misc-difference 108

XX FT /note= "Asp can be replaced with Glu"

XX FT Misc-difference 111

XX FT /note= "Gly can be replaced with Asp"

XX FT Misc-difference 138

XX FT /note= "Trp can be replaced with Ala, Glu, Asp, Asn, Met,

XX Ile, Phe, Tyr, Ser, Thr, Gly, Gln, Val, or Leu; or a

XX pharmaceutically acceptable salt thereof"

XX EP827750-A2.

XX 11-MAR-1998.

XX 22-AUG-1997; 97EP-00306420.

XX 23-AUG-1996; 96US-0024121P.

```

PR 23-AUG-1996; 96US-0025207P.
PA (ELIL ) LILLY & CO ELI.
XX
XX
PI Beals JM, Rinella JV;
XX
XX WPI, 1998-180894/17.
DR
XX
XX Parenteral obesity protein formulations - containing anionic amphiphilic
PT solubiliser and stabilise.
XX
XX Disclosure; Page 9; 45pp; English.
XX
CC The present sequence represents an obesity protein generic formula for
CC producing obesity protein analogues for use in the present invention as
CC part of a soluble parenteral formulation. The soluble parenteral
CC formulations comprises an obesity protein or obesity protein analogue and
CC an anionic amphiphilic compound. The formulations are used for treating
CC obesity and associated disorders. The proteins are preferably present at
CC a concentration of 5-50 mg/ml. The anionic amphiphilic compound
CC solubilises and stabilises the protein
XX
XX Sequence 146 AA;
SQ
    Query Match      100.0%; Score 736; DB 2; Length 146;
    Best Local Similarity 100.0%; Pred. No. 7.8e-73;
    Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKVTGLDFIPGLHPILTISKMDQTILAV 60
   |||||
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKVTGLDFIPGLHPILTISKMDQTILAV 60
   |||||
QY 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETLDSLGGLVLEASGYS 120
   |||||
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETLDSLGGLVLEASGYS 120
   |||||
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
   |||||
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
   |||||

RESULT 15
AA43311
ID AA43311 standard; protein; 146 AA.
XX
XX AC
XX
XX 21-JAN-2000 (first entry)
XX
XX Human leptin.
XX
XX Leptin; brain function improver; brain denaturation disease; therapy;
KW Alzheimer's disease; old age dementia; Pick's disease;
KW hereditary aphasia; Huntington's chorea; Parkinson's disease;
KW progressive subcutaneous gliosis; progressive supranuclear paralysis;
KW thalamus denaturation; myoclonus epilepsy.
XX
XX Homo sapiens.
XX
XX JP11279074-A.
XX
XX 12-OCT-1999.
XX
XX 26-MAR-1998; 98JP-00100202.
XX
XX 26-MAR-1998; 98JP-00100202.
XX
XX (OMUR/) OMURA H.
PA (HORI/) HORI N.
PA (SHIR/) SHIRAIISHI T.
PA (SASA/) SASAKI K.
PA (TAKE/) TAKEDA H.
PA (TSUJ/) TSUJI M.

```

```

PA (MATS/) MATSUMIYA T.
XX
XX WPI; 1999-629222/54.
XX
XX A brain function improver - useful for treating brain disorientation
PT diseases.
XX
XX Disclosure; Page 5; 11pp; Japanese.
XX
XX This sequence represents human leptin. The invention relates to a brain
XX function improver containing mammalian leptin as the active component.
XX The brain function improver is useful as a treating agent for brain
XX denaturation diseases such as Alzheimer's disease, old age dementia,
XX Pick's disease, Huntington's chorea, Parkinson's disease, Parkinson
XX syndrome, progressive subcutaneous gliosis, progressive supranuclear
XX paralysis, thalamus denaturation, hereditary aphasia and myoclonus
XX epilepsy, and other diseases causing deterioration of brain function
XX
XX Sequence 146 AA;
SQ
    Query Match      100.0%; Score 736; DB 2; Length 146;
    Best Local Similarity 100.0%; Pred. No. 7.8e-73;
    Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKVTGLDFIPGLHPILTISKMDQTILAV 60
   |||||
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSQKVTGLDFIPGLHPILTISKMDQTILAV 60
   |||||
QY 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETLDSLGGLVLEASGYS 120
   |||||
Db 61 YQOILTSMPSRNVIQISNDLENLRDLHLVLAFSKSHLPWASGLETLDSLGGLVLEASGYS 120
   |||||
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
   |||||
Db 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
   |||||

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Job time : 118.15 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 28.4537 Seconds
(without alignments)
383.035 Million cell updates/sec

Title: US-10-049-182-6

Perfect score: 736

Sequence: 1 VPIQKVQDDTKTLTKTIVTR.....SRQGSLOQLMLQDLSPGC 146

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Issued Patents AA.*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep.*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep.*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep.*
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5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep.*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	736	100.0	146	1	US-08-398-021-3
2	736	100.0	146	2	US-08-788-943A-5
3	736	100.0	146	2	US-08-823-104-3
4	736	100.0	146	2	US-09-003-081-6
5	736	100.0	146	3	US-08-648-262-6
6	736	100.0	146	3	US-08-648-263-6
7	736	100.0	146	3	US-08-914-375C-32
8	736	100.0	146	4	US-09-172-644-1
9	736	100.0	146	4	US-09-221-178-1
10	736	100.0	146	4	US-09-200-919-1
11	736	100.0	146	5	PCT-US96-00952-2
12	736	100.0	146	5	PCT-US96-00952-3
13	736	100.0	147	4	US-09-200-919-4
14	736	100.0	148	1	US-08-429-362-3
15	736	100.0	148	2	US-08-823-104-18
16	736	100.0	167	2	US-08-540-242A-4
17	736	100.0	167	2	US-08-347-563A-4
18	736	100.0	167	2	US-09-003-081-5
19	736	100.0	167	3	US-08-292-345B-4
20	736	100.0	167	3	US-08-648-262-5
21	736	100.0	167	3	US-08-648-263-5
22	736	100.0	167	3	US-08-488-942A-4
23	736	100.0	167	3	US-08-488-214A-4
24	736	100.0	167	3	US-08-488-208A-4
25	736	100.0	167	3	US-08-759-628-1
26	736	100.0	167	3	US-08-688-908-7
27	736	100.0	167	3	US-08-483-211A-4

28 736 100.0 167 3 US-08-488-223A-4 Sequence 4, Appli
29 736 100.0 167 3 US-09-147-805-4 Sequence 4, Appli
30 736 100.0 167 4 US-08-438-431A-4 Sequence 4, Appli
31 736 100.0 167 4 US-08-488-225A-4 Sequence 4, Appli
32 736 100.0 167 4 US-09-204-730B-4 Sequence 4, Appli
33 736 100.0 167 4 US-09-316-393-4 Sequence 4, Appli
34 736 100.0 167 4 US-09-377-081-17 Sequence 17, Appli
35 736 100.0 167 4 US-09-686-647A-4 Sequence 4, Appli
36 736 100.0 167 5 PCT-US96-01471-4 Sequence 2, Appli
37 736 100.0 397 4 US-08-775-066-2 Sequence 2, Appli
38 733 99.6 146 3 US-08-914-375C-34 Sequence 34, Appli
39 731 99.3 146 2 US-08-788-943A-2 Sequence 2, Appli
40 731 99.3 146 2 US-08-788-943A-3 Sequence 3, Appli
41 731 99.3 146 2 US-08-823-104-11 Sequence 11, Appli
42 731 99.3 146 2 US-08-823-104-12 Sequence 12, Appli
43 731 99.3 146 3 US-08-674-774-3 Sequence 3, Appli
44 731 99.3 147 3 US-08-485-942A-97 Sequence 97, Appli
45 731 99.3 147 3 US-08-488-214A-97 Sequence 97, Appli

ALIGNMENTS

RESULT 1
US-08-398-021-3
; Sequence 3, Application US/08398021
; Patent No. 5594101
; GENERAL INFORMATION:
; APPLICANT: Becker, Gerald W.
; APPLICANT: Hale, John E. Warren C.
; TITLE OF INVENTION: ANTI-OBESITY PROTEINS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/398,021
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10001
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-276-0757
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-398-021-3

Query Match 100.0%; Score 736; DB 1; Length 146;

Best Local Similarity 100.0%; Pred. No. 4e-74; Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLTKTIVTRINDISHTQSVSKQVKGDTGDPGLHPLITLSKMDQTLAV 60

Db 1 VPIQKVQDDTKTLTKTIVTRINDISHTQSVSKQVKGDTGDPGLHPLITLSKMDQTLAV 60

QY 61 YQQLTSPSRNVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
Db 61 YQQLTSPSRNVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRQSGSLQDMLWQLDLSGPC 146
Db 121 TEVALSRQSGSLQDMLWQLDLSGPC 146

RESULT 2

US-08-788-943A-5
; Sequence 5, Application US/08/788943A
; Patent No. 5831017
; GENERAL INFORMATION:
; APPLICANT: Hoffmann, James Arthur
; TITLE OF INVENTION: OBESITY PROTEIN ANALOG COMPOUNDS AND
; TITLE OF INVENTION: FORMULATIONS THEREOF
; NUMBER OF SEQUENCES: 35
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company
; STREET: Lilly Corporate Center/Patent Division
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/788,943A
; FILING DATE: 24-JAN-1997
; CLASSIFICATION: 530
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10540
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-788-943A-5

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLTKTIYTRINDISHTQSVSQKQVTGLDFIPGLHPILTLKMDQTLAV 60
Db 1 VPIQKVQDDTKTLTKTIYTRINDISHTQSVSQKQVTGLDFIPGLHPILTLKMDQTLAV 60
QY 61 YQQLTSPSRNVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
Db 61 YQQLTSPSRNVQISNDLENLRDLHLVLAFAFSKSLPWAAGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRQSGSLQDMLWQLDLSGPC 146
Db 121 TEVALSRQSGSLQDMLWQLDLSGPC 146

RESULT 3

US-08-823-104-3
; Sequence 3, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R

; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: Mackellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 97
; OTHER INFORMATION: /note= "His at position 97 is
; OTHER INFORMATION: replaced with Gln, Asn, Ala, Gly, Ser, or Pro"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 100
; OTHER INFORMATION: /note= "Trp at position 100 is
; OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 101
; OTHER INFORMATION: /note= "Ala at position 101 is
; OTHER INFORMATION: replaced with Ser, Asn, Gly, His, Pro, Thr, or Val"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 102
; OTHER INFORMATION: /note= "Ser at position 102 is
; OTHER INFORMATION: replaced with Arg"
; FEATURE:
; NAME/KEY: Modified-site
; LOCATION: 103
; OTHER INFORMATION: /note= "Gly at position 103 is
; OTHER INFORMATION: replaced with Ala"
; FEATURE:

NAME/KEY: Modified-site
LOCATION: 105
OTHER INFORMATION: /note= "Glu at position 105 is
OTHER INFORMATION: replaced with Gln"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 106
OTHER INFORMATION: /note= "Thr at position 106 is
OTHER INFORMATION: replaced with Lys or Ser"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 107
OTHER INFORMATION: /note= "Leu at position 107 is
OTHER INFORMATION: replaced with Pro"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 111
OTHER INFORMATION: /note= "Gly at position 111 is
OTHER INFORMATION: replaced with Asp"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 118
OTHER INFORMATION: /note= "Gly at position 118 is
OTHER INFORMATION: replaced with Leu"
FEATURE:
NAME/KEY: Modified-site
LOCATION: 138
OTHER INFORMATION: /note= "Trp at position 138 is
OTHER INFORMATION: replaced with Ala, Glu, Asp, Asn, Met, Ser, Thr, or Gly"
US-08-823-104-3

Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQOILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRLOGLQDMLWOLDLSPGC 146
DB 121 TEVALSRLOGLQDMLWOLDLSPGC 146

RESULT 4
US-09-003-081-6
Sequence 6, Application US/09003081
Patent No. 5968779
GENERAL INFORMATION:
APPLICANT: Campfield, Arthur Dr.
APPLICANT: Devos, Rene Dr.
APPLICANT: Guisez, Yves Dr.
TITLE OF INVENTION: Recombinant Obese (OB) Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/003,081
FILING DATE:

CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/435,777
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Picut, Catherine A.
REGISTRATION NUMBER: 37419
REFERENCE/DOCKET NUMBER: 9165
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 6:
SEQUENCE CHARACTERISTICS:
LENGTH: 146 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-09-003-081-6
Query Match 100.0%; Score 736; DB 2; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQVQDDTKLTIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQOILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
DB 61 YQOILTSPSRNVIQISNDLENLRLDLLHLVAFSKSCHLPWASGLETLDLSLGGVLEASGYS 120
QY 121 TEVALSRLOGLQDMLWOLDLSPGC 146
DB 121 TEVALSRLOGLQDMLWOLDLSPGC 146
RESULT 5
US-08-648-262-6
Sequence 6, Application US/08648262
Patent No. 6025324
GENERAL INFORMATION:
APPLICANT: Bailon, Pascal Mr.
APPLICANT: Campfield, Arthur Dr.
APPLICANT: Devos, Rene Dr.
APPLICANT: Guisez, Yves Dr.
TITLE OF INVENTION: Pegylated Obese (OB) Proteins
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: Hoffmann-La Roche, Inc.
STREET: 340 Kingsland Street
CITY: Nutley
STATE: New Jersey
COUNTRY: U.S.A.
ZIP: 07110
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/648,262
FILING DATE:
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Epstein, William H.
REGISTRATION NUMBER: 20008
REFERENCE/DOCKET NUMBER: 9281
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-3723
TELEFAX: (201) 235-2363

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; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-648-262-6

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 6
US-08-648-263-6
; Sequence 6, Application US/08648263
; Patent No. 6025325
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur
; APPLICANT: Devos, Rene
; TITLE OF INVENTION: RECOMBINANT OBESE (OB) PROTEINS
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; OPERATING SYSTEM: IBM PC compatible
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/648,263
; FILING DATE: 15-MAY-1996
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/484,629
; FILING DATE: 07-JUN-1995
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/435,777
; FILING DATE: 05-MAY-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Kreisler, Lewis J
; REGISTRATION NUMBER: 38522
; REFERENCE/DOCKET NUMBER: RAN 4105/175-002
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201)235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown

; INFORMATION FOR SEQ ID NO: 6:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown

; MOLECULE TYPE: peptide
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
US-08-648-263-6

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 7
US-08-914-375C-32
; Sequence 32, Application US/08914375C
; Patent No. 6377893
; GENERAL INFORMATION:
; APPLICANT: Steven A. Benner
; NUMBER OF SEQUENCES: 74
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Steven A. Benner
; STREET: 1501 NW 68th Terrace
; CITY: Gainesville
; STATE: FL
; COUNTRY: United States
; ZIP: 32605-4147
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch diskette
; OPERATING SYSTEM: Macintosh
; SOFTWARE: Microsoft Word
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/914,375C
; FILING DATE: 19-Aug-1997
; CLASSIFICATION: 702/20
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 352 392 7773
; TELEFAX: 352 331 0462
; INFORMATION FOR SEQ ID NO: 32:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: amino acid
; ORIGINAL SOURCE:
; ORGANISM: human
; FEATURE:
; OTHER INFORMATION: leptin
; SEQUENCE DESCRIPTION: SEQ ID NO: 32:
US-08-914-375C-32

Query Match      100.0%; Score 736; DB 3; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 1 VPIQKQVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
QY 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVIQISNDLENLRDLHLVLAFAFSKCHLPWASGLETLDSLGGVLEASGYS 120
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Qy 121 TEVALSRLOGSLQDMLWQLDLSPEC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSPEC 146

RESULT 8
US-09-172-644-1
; Sequence 1, Application US/09172644
; Patent No. 6420339
; GENERAL INFORMATION:
; APPLICANT: KINSTLER, OLAF
; TITLE OF INVENTION: SITE-DIRECTED DUAL PEGLATION OF PROTEINS FOR IMPROVED
; FILE REFERENCE: A-567
; CURRENT APPLICATION NUMBER: US/09/172,644
; CURRENT FILING DATE: 1998-10-14
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-172-644-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Qy 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRLOGSLQDMLWQLDLSPEC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSPEC 146

RESULT 9
US-09-221-178-1
; Sequence 1, Application US/09221178
; Patent No. 6451346
; GENERAL INFORMATION:
; APPLICANT: SHAH, SUBODH
; APPLICANT: DAI, WEIGUO
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/09/221,178
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-09-221-178-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Qy 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRLOGSLQDMLWQLDLSPEC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSPEC 146

RESULT 10
US-09-200-919-1
; Sequence 1, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: COMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAIISHI, TAKEMASA
; APPLICANT: SASAKI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJIT, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100
; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-1

Query Match 100.0%; Score 736; DB 4; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLSKMDQTLAV 60
Qy 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIOISNDLENLRDLHLVLAFSKCHLPWASGLETLDSLGVLASGYS 120
Qy 121 TEVALSRLOGSLQDMLWQLDLSPEC 146
Db 121 TEVALSRLOGSLQDMLWQLDLSPEC 146

RESULT 11
PCT-US96-00952-2
; Sequence 2, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00952-2
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Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 12

PCT-US96-00952-3
; Sequence 3, Application PC/TUS9600952
; GENERAL INFORMATION:
; APPLICANT:
; TITLE OF INVENTION: Anti-Obesity Proteins
; NUMBER OF SEQUENCES: 16
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: PCT/US96/00952
; FILING DATE:
; CLASSIFICATION:
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 146 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
PCT-US96-00952-3

Query Match 100.0%; Score 736; DB 5; Length 146;
Best Local Similarity 100.0%; Pred. No. 4e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
DB 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 120
DB 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 120
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
DB 121 TEVALSRLOGSLQDMLWQLDLSGPC 146

RESULT 13

US-09-200-919-4
; Sequence 4, Application US/09200919
; Patent No. 6518235
; GENERAL INFORMATION:
; APPLICANT: OOMURA, YUTAKA
; APPLICANT: HORI, NOBUAKI
; APPLICANT: SHIRAI, TAKEMASA
; APPLICANT: SAKAI, KAZUO
; APPLICANT: TAKEDA, HIROSHI
; APPLICANT: TSUJI, MINORU
; APPLICANT: MATSUMIYA, TERUHIKO
; TITLE OF INVENTION: DRUG FOR IMPROVEMENT OF BRAIN FUNCTION
; FILE REFERENCE: YAMA-100

; CURRENT APPLICATION NUMBER: US/09/200,919
; CURRENT FILING DATE: 1998-11-30
; NUMBER OF SEQ ID NOS: 6
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 4
; LENGTH: 147
; TYPE: PRT
; ORGANISM: HUMAN
US-09-200-919-4

Query Match 100.0%; Score 736; DB 4; Length 147;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 2 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 61
QY 61 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 120
DB 62 YQQLTSMPSRNVQISNDLENLRLDLHLVLAFAFSKSLPWLASGLETLDSLGGVLEASGYS 121
QY 121 TEVALSRLOGSLQDMLWQLDLSGPC 146
DB 122 TEVALSRLOGSLQDMLWQLDLSGPC 147

RESULT 14

US-08-429-362-3
; Sequence 3, Application US/08429362
; Patent No. 5614379
; GENERAL INFORMATION:
; APPLICANT: Mackellar, Warren C.
; TITLE OF INVENTION: Process For Preparing Anti-Obesity
; TITLE OF INVENTION: Protein
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly and Company/Patent Division
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: United States
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/429,362
; FILING DATE:
; CLASSIFICATION:
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P.
; REGISTRATION NUMBER: 36,467
; REFERENCE/DOCKET NUMBER: X10022
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (317) 276-0757
; TELEFAX: (317) 277-1917
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-429-362-3

Query Match 100.0%; Score 736; DB 1; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Db 3 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
Qy 61 YQOILTSPSRNVIQISNDLENRLDLLHLVLAFAFSKSLPWPASGLETLDSLGGVLEASGYS 120
Db 63 YQOILTSPSRNVIQISNDLENRLDLLHLVLAFAFSKSLPWPASGLETLDSLGGVLEASGYS 122
Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 123 TEVVALSRLOGLQDMLWQLDLSFGC 148

RESULT 15

US-08-823-104-18
; Sequence 18, Application US/08823104
; Patent No. 5840517
; GENERAL INFORMATION:
; APPLICANT: Atkinson, Paul R
; APPLICANT: Foster, Lisa K
; APPLICANT: Furman, Thomas C
; APPLICANT: Mackellar, Warren C
; TITLE OF INVENTION: Process for Preparing Obesity Protein
; TITLE OF INVENTION: Analogs
; NUMBER OF SEQUENCES: 18
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Eli Lilly & Company
; STREET: Lilly Corporate Center
; CITY: Indianapolis
; STATE: Indiana
; COUNTRY: USA
; ZIP: 46285
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent In Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/823,104
; FILING DATE: 24-MAR-1997
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US 08/429,362
; FILING DATE: 26-APR-1995
; ATTORNEY/AGENT INFORMATION:
; NAME: Caltrider, Steven P
; REGISTRATION NUMBER: 36467
; REFERENCE/DOCKET NUMBER: 10022A
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 317-277-8110
; TELEFAX: 317-277-1917
; INFORMATION FOR SEQ ID NO: 18:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 148 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; HYPOTHETICAL: NO
; ANTI-SENSE: NO
; FRAGMENT TYPE: N-terminal
US-08-823-104-18

Query Match 100.0%; Score 736; DB 2; Length 148;
Best Local Similarity 100.0%; Pred. No. 4.1e-74;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 3 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSKQKVTGLDFIPGLHPILTLTKMDQTLAV 62
Qy 61 YQOILTSPSRNVIQISNDLENRLDLLHLVLAFAFSKSLPWPASGLETLDSLGGVLEASGYS 120
Db 63 YQOILTSPSRNVIQISNDLENRLDLLHLVLAFAFSKSLPWPASGLETLDSLGGVLEASGYS 122

Qy 121 TEVVALSRLOGLQDMLWQLDLSFGC 146
Db 123 TEVVALSRLOGLQDMLWQLDLSFGC 148

Search completed: March 12, 2005, 05:05:40
Job time : 29.4537 secs

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OM protein - protein search, using sw model

Run on: March 12, 2005, 05:03:46 ; Search time 82.0958 Seconds
(without alignments)
586.599 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQVQDDTKTLIKTIIVTR.....SRLOGSLQDMLWQLDLSFGC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

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11: /cgn2_6/ptodata/1/pubpaa/US09C_PUBCOMB.pep.*
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16: /cgn2_6/ptodata/1/pubpaa/US10D_PUBCOMB.pep.*
17: /cgn2_6/ptodata/1/pubpaa/US10_NEW_PUB.pep.*
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19: /cgn2_6/ptodata/1/pubpaa/US60_NEW_PUB.pep.*
20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	146	14	US-10-191-377-1
2	736	100.0	146	15	US-10-139-794-10
3	736	100.0	146	15	US-10-419-058-2
4	736	100.0	146	15	US-10-467-114-1
5	736	100.0	146	16	US-10-622-998-1
6	736	100.0	146	16	US-10-658-834A-211
7	736	100.0	146	16	US-10-468-496-1
8	736	100.0	146	17	US-10-872-198-127
9	736	100.0	146	17	US-10-623-189-1
10	736	100.0	167	9	US-09-736-084-4
11	736	100.0	167	9	US-09-928-522-7
12	736	100.0	167	9	US-09-789-306-3
13	736	100.0	167	9	US-09-804-409A-11

14	736	100.0	167	10	US-09-316-393-4	Sequence 4, Appli
15	736	100.0	167	15	US-10-440-464-67	Sequence 67, Appli
16	736	100.0	167	15	US-10-458-334-17	Sequence 17, Appli
17	736	100.0	167	17	US-10-698-510-17	Sequence 17, Appli
18	736	100.0	374	15	US-10-679-999-15	Sequence 15, Appli
19	736	100.0	374	15	US-10-679-999-18	Sequence 18, Appli
20	736	100.0	379	15	US-10-679-999-9	Sequence 9, Appli
21	736	100.0	379	15	US-10-679-999-12	Sequence 12, Appli
22	736	100.0	396	9	US-09-859-361-2	Sequence 2, Appli
23	736	100.0	396	9	US-09-859-361-5	Sequence 5, Appli
24	736	100.0	397	8	US-08-779-457-47	Sequence 47, Appli
25	736	100.0	397	17	US-10-921-710-47	Sequence 47, Appli
26	736	100.0	399	9	US-09-859-361-7	Sequence 7, Appli
27	736	100.0	401	9	US-09-859-361-9	Sequence 9, Appli
28	734	99.7	146	16	US-10-658-834A-666	Sequence 666, App
29	734	99.7	146	16	US-10-658-834A-672	Sequence 672, App
30	734	99.7	146	16	US-10-658-834A-677	Sequence 677, App
31	734	99.7	146	16	US-10-658-834A-683	Sequence 683, App
32	733	99.6	146	16	US-10-658-834A-665	Sequence 665, App
33	733	99.6	146	16	US-10-658-834A-671	Sequence 671, App
34	733	99.6	146	16	US-10-658-834A-673	Sequence 673, App
35	733	99.6	146	16	US-10-658-834A-676	Sequence 676, App
36	733	99.6	146	16	US-10-658-834A-682	Sequence 682, App
37	731	99.3	146	9	US-09-850-433-4	Sequence 4, Appli
38	731	99.3	146	16	US-10-658-834A-674	Sequence 674, App
39	731	99.3	146	16	US-10-658-834A-675	Sequence 675, App
40	731	99.3	146	16	US-10-658-834A-679	Sequence 679, App
41	731	99.3	146	16	US-10-658-834A-681	Sequence 681, App
42	731	99.3	147	9	US-09-366-133-6	Sequence 6, Appli
43	731	99.3	147	9	US-09-736-084-97	Sequence 97, Appli
44	731	99.3	147	9	US-09-853-768-4	Sequence 4, Appli
45	731	99.3	147	10	US-09-094-931-4	Sequence 4, Appli

ALIGNMENTS

RESULT 1
US-10-191-377-1
; Sequence 1, Application US/10191377
; Publication No. US20030099709A1
; GENERAL INFORMATION:
; APPLICANT: AMGEN INC.
; TITLE OF INVENTION: BIODEGRADABLE, pH/THERMOSENSITIVE HYDROGEL FOR
; FILE REFERENCE: A-575
; CURRENT APPLICATION NUMBER: US/10/191,377
; CURRENT FILING DATE: 1998-12-23
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: Patent in Ver. 2.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Human Leptin
US-10-191-377-1

Query Match 100.0%; Score 736; DB 14; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy	1	VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV	60
Db	1	VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV	60
Qy	61	YQOILTSMPNRNVIQISNDLENRLDLHLVLAFLSKCHLPWASGLTDLGGLVLEASGYS	120
Db	61	YQOILTSMPNRNVIQISNDLENRLDLHLVLAFLSKCHLPWASGLTDLGGLVLEASGYS	120
Qy	121	TEVALSRLOGSLQDMLWQLDLSFGC	146
Db	121	TEVALSRLOGSLQDMLWQLDLSFGC	146

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RESULT 2
US-10-139-794-10
; Sequence 10, Application US/10139794
; Publication No. US20030232421A1
; GENERAL INFORMATION:
; APPLICANT: HYBRIGENICS, LYNX THERAPEUTICS INC.
; APPLICANT: Pierre Legrain, Simon Whiteside, Jen-I Mao, Irina Khrebtukova, Shujun Luo
; TITLE OF INVENTION: Protein-Protein Interactions In Adipocyte Cells (3)
; FILE REFERENCE: B4883A
; CURRENT APPLICATION NUMBER: US/10/139,794
; CURRENT FILING DATE: 2002-05-06
; PRIOR APPLICATION NUMBER: US 60/288,885
; PRIOR FILING DATE: 2001-05-04
; NUMBER OF SEQ ID NOS: 2930
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 10
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
; FEATURE:
; OTHER INFORMATION: Translation of SEQ ID NO:9
US-10-139-794-10

Query Match 100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 3
US-10-419-058-2
; Sequence 2, Application US/10419058
; Publication No. US20040053366A1
; GENERAL INFORMATION:
; APPLICANT: Lo, Kin-Ming
; APPLICANT: Zhang, Jinyang
; APPLICANT: Gillies, Stephen D.
; TITLE OF INVENTION: Expression and Export of Anti-Obesity Proteins as Fc
; FILE REFERENCE: LEX-008
; CURRENT APPLICATION NUMBER: US/10/419,058
; CURRENT FILING DATE: 2003-04-18
; PRIOR APPLICATION NUMBER: US/09/479,508
; PRIOR FILING DATE: 2000-01-07
; PRIOR FILING DATE: 1999-01-07
; NUMBER OF SEQ ID NOS: 20
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 2
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-419-058-2

Query Match 100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 4
US-10-467-114-1
; Sequence 1, Application US/10467114
; Publication No. US20040072219A1
; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: MODIFIED LEPTIN WITH REDUCED
; TITLE OF INVENTION: IMMUNOGENICITY
; FILE REFERENCE: MER-115
; CURRENT APPLICATION NUMBER: US/10/467,114
; CURRENT FILING DATE: 2003-08-05
; PRIOR APPLICATION NUMBER: EP 01102618.4
; PRIOR FILING DATE: 2001-02-06
; PRIOR APPLICATION NUMBER: EP 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: PCT/EP02/01188
; PRIOR FILING DATE: 2002-02-05
; NUMBER OF SEQ ID NOS: 52
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapien
US-10-467-114-1

Query Match 100.0%; Score 736; DB 15; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTILSKMDQTLAV 60

Qy 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 61 YQOILTSMPSRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGGVLEASGYS 120

Qy 121 TEVALSRLOGLQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLQDMLWQLDLSGPC 146

RESULT 5
US-10-622-998-1
; Sequence 1, Application US/10622998
; Publication No. US20040105840A1
; GENERAL INFORMATION:
; APPLICANT: Kinstler, Olaf
; APPLICANT: Ladd, David
; APPLICANT: Papisov, Mikhail
; TITLE OF INVENTION: PROTEIN CONJUGATES WITH A WATER-SOLUBLE BIOCOMPATIBLE, BIODEGRADABLE
; FILE REFERENCE: A-822
; CURRENT APPLICATION NUMBER: US/10/622,998
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: 60/397,509
; PRIOR FILING DATE: 2002-07-19
; NUMBER OF SEQ ID NOS: 1
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
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; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-622-998-1

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120

QY 121 TEVVALSRLOGLSQDMLWQDLSPGC 146
Db 121 TEVVALSRLOGLSQDMLWQDLSPGC 146

RESULT 6
US-10-658-834A-211
; Sequence 211, Application US/10658834A
; Publication No. US20040132977A1
; GENERAL INFORMATION:
; APPLICANT: Gantier, Rene
; APPLICANT: Guyon, Thierry
; APPLICANT: Dritanti, Lila
; APPLICANT: Vega, Manuel
; TITLE OF INVENTION: Rational Evolution of Cytokines for Higher Stability, Encoding Nu
; TITLE OF INVENTION: Acid
; FILE REFERENCE: 38751-922
; CURRENT APPLICATION NUMBER: US/10/658,834A
; PRIOR FILING DATE: 2003-09-08
; PRIOR APPLICATION NUMBER: 60/457,135
; PRIOR FILING DATE: 2003-03-21
; PRIOR APPLICATION NUMBER: 60/409,898
; PRIOR FILING DATE: 2002-09-09
; NUMBER OF SEQ ID NOS: 1306
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 211
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
; PUBLICATION INFORMATION:
; DATABASE ACCESSION NUMBER: Genbank AAA60470
; DATABASE ENTRY DATE: 1995-01-13
US-10-658-834A-211

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120

QY 121 TEVVALSRLOGLSQDMLWQDLSPGC 146
Db 121 TEVVALSRLOGLSQDMLWQDLSPGC 146

RESULT 7
US-10-468-496-1
; Sequence 1, Application US/10468496
; Publication No. US20040180386A1

; GENERAL INFORMATION:
; APPLICANT: Carr, Francis J.
; APPLICANT: Carter, Graham
; APPLICANT: Jones, Tim
; APPLICANT: Williams, Stephen
; APPLICANT: Hamilton, Anita
; TITLE OF INVENTION: METHOD FOR IDENTIFICATION OF T-CELL
; TITLE OF INVENTION: EPITOPES AND USE FOR PREPARING MOLECULES WITH REDUCED
; FILE REFERENCE: MER-117
; CURRENT APPLICATION NUMBER: US/10/468,496
; CURRENT FILING DATE: 2003-09-25
; PRIOR APPLICATION NUMBER: 01103954.2
; PRIOR FILING DATE: 2001-02-19
; PRIOR APPLICATION NUMBER: 01105777.5
; PRIOR FILING DATE: 2001-03-08
; PRIOR APPLICATION NUMBER: 01106538.0
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01106536.4
; PRIOR FILING DATE: 2001-03-15
; PRIOR APPLICATION NUMBER: 01107012.5
; PRIOR FILING DATE: 2001-03-20
; PRIOR APPLICATION NUMBER: 01106899.6
; PRIOR FILING DATE: 2001-03-20
; NUMBER OF SEQ ID NOS: 2036
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo Sapiens
US-10-468-496-1

Query Match      100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120
Db 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSCHPWASGLETLDSLGVLASGYS 120

QY 121 TEVVALSRLOGLSQDMLWQDLSPGC 146
Db 121 TEVVALSRLOGLSQDMLWQDLSPGC 146

RESULT 8
US-10-872-198-127
; Sequence 127, Application US/10872198
; Publication No. US20050002897A1
; GENERAL INFORMATION:
; APPLICANT: Ulrich HAUPTS
; APPLICANT: Andre KOLTERMANN
; APPLICANT: Andreas SCHEIDIG
; APPLICANT: Christian VOETSMER
; APPLICANT: Ulrich Ketting
; TITLE OF INVENTION: NEW BIOLOGICAL ENTITIES AND USE THEREOF
; FILE REFERENCE: 04156.000204
; CURRENT APPLICATION NUMBER: US/10/872,198
; CURRENT FILING DATE: 2004-06-18
; PRIOR APPLICATION NUMBER: 60/543,518
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: 60/524,960
; PRIOR FILING DATE: 2003-11-25
; PRIOR APPLICATION NUMBER: EP 04003058
; PRIOR FILING DATE: 2004-02-11
; PRIOR APPLICATION NUMBER: EP 03025871
; PRIOR FILING DATE: 2003-11-11
; PRIOR APPLICATION NUMBER: EP 03025851
; PRIOR FILING DATE: 2003-11-10
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; PRIOR APPLICATION NUMBER: EP 03013819
; PRIOR FILING DATE: 2003-06-18
; NUMBER OF SEQ ID NOS: 149
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 127
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-872-198-127

Query Match 100.0%; Score 736; DB 16; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146
DB 121 TEVVALSRQGSLOQDMWLQDLSPGC 146

RESULT 9

US-10-623-189-1
; Sequence 1, Application US/10623189
; Publication No. US20050020496A1
; GENERAL INFORMATION:
; APPLICANT: DEPAOLI, Alex M.
; APPLICANT: ORAL, Elif Arioglu
; APPLICANT: TAYLOR, Simeon I.
; APPLICANT: GARG, Abhimanyu
; TITLE OF INVENTION: USE OF LEPTIN FOR TREATING HUMAN LIPOATROPHY AND METHOD OF DETERM
; FILE REFERENCE: 54113.8005.US02
; CURRENT APPLICATION NUMBER: US/10/623,189
; CURRENT FILING DATE: 2003-07-18
; PRIOR APPLICATION NUMBER: US 10/279,129
; PRIOR FILING DATE: 2002-10-22
; PRIOR APPLICATION NUMBER: US 60/336,394
; PRIOR FILING DATE: 2001-10-22
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: PatentIn version 3.1
; SEQ ID NO 1
; LENGTH: 146
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE:
; OTHER INFORMATION: Recombinant Leptin Human 146 (rHu-Leptin 1-146)
US-10-623-189-1

Query Match 100.0%; Score 736; DB 17; Length 146;
Best Local Similarity 100.0%; Pred. No. 3.2e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146
DB 121 TEVVALSRQGSLOQDMWLQDLSPGC 146

RESULT 10

US-09-928-522-7

; Sequence 7, Application US/09928522

; Patent No. US20020110857A1

; GENERAL INFORMATION:

; APPLICANT: Spurlock, Michael E.

US-09-736-084-4

; Sequence 4, Application US/09736084

; Patent No. US20020107211A1

; GENERAL INFORMATION:

; APPLICANT: THE ROCKEFELLER UNIVERSITY

; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

; NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

; NUMBER OF SEQUENCES: 98

; CORRESPONDENCE ADDRESS:

; ADDRESSEE: Klauber & Jackson

; STREET: 411 Hackensack Avenue

; CITY: Hackensack

; STATE: New Jersey

; COUNTRY: USA

; ZIP: 07601

; COMPUTER READABLE FORM:

; MEDIUM TYPE: Floppy disk

; COMPUTER: IBM PC compatible

; OPERATING SYSTEM: PC-DOS/MS-DOS

; SOFTWARE: PatentIn Release #1.0, Version #1.25

; CURRENT APPLICATION DATA:

; APPLICATION NUMBER: US/09/736,084

; FILING DATE: 13-Dec-2000

; CLASSIFICATION: <Unknown>

; PRIOR APPLICATION DATA:

; APPLICATION NUMBER: 08/438,431

; FILING DATE: May 10, 1995

; APPLICATION NUMBER: 08/347,563

; FILING DATE: No. US20020107211A1, September 30, 1994

; APPLICATION NUMBER: 08/292,345

; FILING DATE: August 17, 1994

; ATTORNEY/AGENT INFORMATION:

; NAME: Jackson Esq., David A.

; REGISTRATION NUMBER: 26,742

; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21

; TELECOMMUNICATION INFORMATION:

; TELEPHONE: 201 487-5800

; TELEFAX: 201 343-1684

; TELEX: 133521

; INFORMATION FOR SEQ ID NO: 4:

; SEQUENCE CHARACTERISTICS:

; LENGTH: 167 amino acids

; TYPE: amino acid

; TOPOLOGY: linear

; MOLECULE TYPE: protein

; DESCRIPTION: Human ob polypeptide

; ORIGINAL SOURCE:

; SEQUENCE DESCRIPTION: SEQ ID NO: 4:

US-09-736-084-4

Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILITLSKMDQTLAV 81

QY 61 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
DB 82 YQOILTSMPSRNVQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGGLVLEASGYS 141

QY 121 TEVVALSRQGSLOQDMWLQDLSPGC 146
DB 142 TEVVALSRQGSLOQDMWLQDLSPGC 167

RESULT 11

US-09-928-522-7

; Sequence 7, Application US/09928522

; Patent No. US20020110857A1

; GENERAL INFORMATION:

; APPLICANT: Spurlock, Michael E.

;; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
;; SEQUENCES CODING THEREFOR AND USES THEREOF
;; NUMBER OF SEQUENCES: 8
;; CORRESPONDENCE ADDRESS:
;; ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
;; STREET: Suite 2100 111 East Wisconsin Avenue
;; CITY: Milwaukee
;; STATE: Wisconsin
;; COUNTRY: USA
;; ZIP: 53202
;;
;; COMPUTER READABLE FORM:
;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/928,522
;; FILING DATE: 13-Aug-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: US/08/688,908
;; FILING DATE: 31-JUL-1996
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Plotecher, Gary R.
;; REGISTRATION NUMBER: 27,830
;; REFERENCE/DOCKET NUMBER: PM-8808
;; TELECOMMUNICATION INFORMATION:
;; TELEPHONE: 414-273-2100
;; TELEFAX: 414-223-5000
;; INFORMATION FOR SEQ ID NO: 7:
;;
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 167 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: <Unknown>
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-928-522-7

Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLSEAGYS 120
Db 82 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLSEAGYS 141

QY 121 TEVALSRLOQSLQDMLWQLDLSGPC 146
Db 142 TEVALSRLOQSLQDMLWQLDLSGPC 167

RESULT 12
US-09-789-306-3
; Sequence 3, Application US/09789306
; Patent No. US20020142456A1
; GENERAL INFORMATION:
; APPLICANT: Hernday, Natasha
; TITLE OF INVENTION: Canine OB Protein Compositions and Methods
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:

;; MEDIUM TYPE: Floppy disk
;; COMPUTER: IBM PC compatible
;; OPERATING SYSTEM: PC-DOS/MS-DOS
;; SOFTWARE: Patent In Release #1.0, Version #1.30
;; CURRENT APPLICATION DATA:
;; APPLICATION NUMBER: US/09/789,306
;; FILING DATE: 20-Feb-2001
;; CLASSIFICATION: <Unknown>
;; PRIOR APPLICATION DATA:
;; APPLICATION NUMBER: 08/609,408
;; FILING DATE: <Unknown>
;; ATTORNEY/AGENT INFORMATION:
;; NAME: Eggert, Joan D.
;; REFERENCE/DOCKET NUMBER: A-387
;; INFORMATION FOR SEQ ID NO: 3:
;; SEQUENCE CHARACTERISTICS:
;; LENGTH: 167 amino acids
;; TYPE: amino acid
;; STRANDEDNESS: single
;; TOPOLOGY: linear
;; MOLECULE TYPE: protein
;; FEATURE:
;; NAME/KEY: Leader Sequence
;; LOCATION: -21 to -1
;; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-789-306-3

Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLSEAGYS 120
Db 82 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLSEAGYS 141

QY 121 TEVALSRLOQSLQDMLWQLDLSGPC 146
Db 142 TEVALSRLOQSLQDMLWQLDLSGPC 167

RESULT 13
US-09-804-409A-11
; Sequence 11, Application US/09804409A
; Patent No. US2002015100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: Patent In Ver. 2.1
; SEQ ID NO 11
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-09-804-409A-11

Query Match 100.0%; Score 736; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 22 VPIQVQDDTKTLIKTIIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQOILTSMPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLDSLGVLSEAGYS 120

Db 82 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141
121 TEVALSRLOGLQSLQDMLWQLDLSFGC 146
Db 142 TEVALSRLOGLQSLQDMLWQLDLSFGC 167
RESULT 14
US-09-316-393-4
; Sequence 4, Application US/09316393
; Publication No. US20030040039A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; FILE REFERENCE: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/316,393
; FILING DATE:
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human Ob protein
; ORIGINAL SOURCE: Human
US-09-316-393-4

Query Match 100.0%; Score 736; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLTKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPITLTLKMDQTLAV 60
Db 22 VPIQKVDDTKTLTKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPITLTLKMDQTLAV 81
Qy 61 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 82 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141
Qy 121 TEVALSRLOGLQSLQDMLWQLDLSFGC 146
Db 142 TEVALSRLOGLQSLQDMLWQLDLSFGC 167

RESULT 15
US-10-440-464-67

; Sequence 67, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; FILE REFERENCE: AND ACTIVITY IN MAMMALS
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-67
Query Match 100.0%; Score 736; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 3.8e-72;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 VPIQKVDDTKTLTKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPITLTLKMDQTLAV 60
Db 22 VPIQKVDDTKTLTKTIVTRINDISHTQSVSSKOKVTGLDFIPGLHPITLTLKMDQTLAV 81
Qy 61 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 120
Db 82 YQIILTSMPSRNVIQISNDLENRLDLHLVAFSKSCHLPWASGLETLDSLGVLASGYS 141
Qy 121 TEVALSRLOGLQSLQDMLWQLDLSFGC 146
Db 142 TEVALSRLOGLQSLQDMLWQLDLSFGC 167
Search completed: March 12, 2005, 05:21:04
Job time : 83.0958 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:02 ; Search time 22.8562 Seconds
(without alignments)
614.609 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQKVDKTLIKTIVTR.....SRLQSLQDMLWQLDLSGPC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : PIR 79:*
1: piri:*
2: pir2:*
3: pir3:*
4: pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	167	1 LTHU	leptin precursor -
2	720.5	97.9	166	2 I53166	leptin precursor -
3	619	84.1	167	1 LTMS	leptin precursor -
4	605	82.2	167	1 LTRI	leptin precursor -
5	605	82.2	167	2 I55622	rat ob - rat
6	81.5	11.1	1600	2 AB3281	glutamate dehydrog
7	80.5	10.9	444	2 S54039	hypothetical prote
8	79	10.7	829	2 T01362	probable myosin he
9	79	10.7	952	2 H84583	hypothetical prote
10	78	10.6	450	2 S75514	sensory transducti
11	78	10.6	639	2 AI0055	probable soluble l
12	77.5	10.5	574	1 B42374	phosphotransferase
13	76.5	10.4	173	2 S77486	ribosomal protein
14	76.5	10.4	362	2 A83967	carbamoyl-phosphat
15	76.5	10.4	822	2 E86305	probable trehalase
16	76	10.3	409	2 B89954	hypothetical prote
17	76	10.3	570	2 T46011	hypothetical prote
18	76	10.3	1036	2 D70117	acriflavine resist
19	75.5	10.3	403	2 T26551	hypothetical prote
20	75.5	10.3	1438	2 S59792	probable membrane
21	75	10.2	142	2 C72430	hypothetical prote
22	75	10.2	296	2 D70424	hypothetical prote
23	75	10.2	424	2 E81358	glutamate-1-semial
24	75	10.2	1191	2 S76414	beta transducin-li
25	74.5	10.1	559	2 AB2202	hypothetical prote
26	74.5	10.1	674	2 S46092	probable membrane
27	74	10.1	177	2 A28106	prolactin, 20K - M
28	74	10.1	200	2 B32477	prolactin II precu
29	74	10.1	421	2 AB2959	exopolysaccharide

ALIGNMENTS

RESULT 1

LTHU
leptin precursor - human
N;Alternate names: obese protein; obesity factor
C;Species: Homo sapiens (man)
C;Date: 28-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C;Accession: A38952; J0148
R;Zhang, Y.; Proenca, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A;Title: Positional cloning of the mouse obese gene and its human homologue.
A;Reference number: S50863; MUID:95075453; PMID:7984236
A;Accession: A38952
A;Status: preliminary; nucleic acid sequence not shown
A;Molecule type: mRNA
A;Residues: 1-167 <ZHA>
A;Cross-references: UNIPROT:P41159; GB:U18915; NID:G623331; PIDN:AAA60470.1; PID:G62333
R;Liao, H.J.; Deng, Y.B.; Chen, X.M.; Ye, Y.Z.
Chinese Biochem. J. 13, 249-253, 1997
A;Title: Cloning of chinese obesity gene and construction of prokaryotic expression vec
A;Reference number: JE0148
A;Accession: JE0148
A;Molecule type: mRNA
A;Residues: 'M',22-167 <LTA>
A;Experimental source: adipose
A;Note: the author translated GAC for residue 148 as Ser
C;Genetics:
A;Gene: GDB:LEP; OB; OBS
A;Cross-references: GDB:136420; OMIM:164160
A;Map position: 7q31.3-7q31.3
C;Superfamily: leptin
C;Keywords: adipose tissue
F;1-21/Domain: signal sequence #status predicted <SIG>
F;22-167/Product: leptin #status predicted <MAT>

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.8e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIQKVDKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLKMDQTLAV 81
QY 61 YQOILTSMPSRNVQISNDLENLRLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 120
DB 82 YQOILTSMPSRNVQISNDLENLRLHLVAFSKSCHLPWASGLETLDLSGGVLEASGYS 141
QY 121 TEVVALSRQGSLODMLWQLDLSGPC 146
DB 142 TEVVALSRQGSLODMLWQLDLSGPC 167

RESULT 2

```
153166
leptin precursor - human
N:Alternate names: obese
C:Species: Homo sapiens (man)
C>Date: 01-Nov-1996 #sequence_revision 01-Nov-1996 #text_change 09-Jul-2004
C:Accession: I53166; G02328
R:Masuzaki, H.; Ogawa, Y.; Isse, N.; Satoh, N.; Okazaki, T.; Shigemoto, M.; Mori, K.; Ta
Diabetes 44, 855-858, 1995
A:Title: Human obese gene expression. Adipocyte-specific expression and regional differe
A:Reference number: I53166; MUID:95309556; PMID:7789654
A:Accession: I53166
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-166 <RES>
A:Cross-references: UNIPROT:P41159; GB:D49487; NID:g904211; PIDN:BAA08448.1; PID:g904212
R:Chehab, F.F.; Lim, M.E.
submitted to the EMBL Data Library, December 1995
A:Reference number: H01063
A:Accession: G02328
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-166 <CHE>
A:Cross-references: EMBL:U43415; NID:g1163105; PIDN:AAC31660.1; PID:g1163106
C:Genetics:
A:Gene: GDB:IDP; OB; OBS
A:Cross-references: GDB:136420; OMIM:164160
A:Map position: 7q32.1-7q32.1
A:Introns: 48/3
C:Superfamily: leptin

Query Match 97.9%; Score 720.5; DB 2; Length 166;
Best Local Similarity 99.3%; Pred. No. 4.6e-58;
Matches 145; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHT-SVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 80
QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 81 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 140
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 141 TEVVALSRLOGLQDMLWQLDLSGPC 166

RESULT 3
LIMS
leptin precursor - mouse
N:Alternate names: obese protein
C:Species: Mus musculus (house mouse)
C>Date: 14-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: S50863
R:Zhang, Y.; Piroenka, R.; Maffei, M.; Barone, M.; Leopold, L.; Friedman, J.M.
Nature 372, 425-432, 1994
A:Title: Positional cloning of the mouse obese gene and its human homologue.
A:Reference number: S50863; MUID:95075453; PMID:7984236
A:Accession: S50863
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <ZHA>
A:Cross-references: UNIPROT:P41160; EMBL:U18812; NID:g746416; PIDN:AAA64564.1; PID:g6032
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 84.1%; Score 619; DB 1; Length 167;
Best Local Similarity 84.9%; Pred. No. 7.1e-49;
Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
```

```
Db 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSAKQRTVGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 82 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 4
LIMS
leptin precursor - rat
N:Alternate names: obese protein; obesity factor
C:Species: Rattus norvegicus (Norway rat)
C>Date: 21-Jul-1995 #sequence_revision 16-Aug-1996 #text_change 09-Jul-2004
C:Accession: PC4034; JC4142
R:Funahashi, T.; Shimomura, I.; Hiraoka, H.; Arai, T.; Takahashi, M.; Nakamura, T.; Noz;
Biochem. Biophys. Res. Commun. 211, 469-475, 1995
A:Title: Enhanced expression of rat obese (Ob) gene in adipose tissues of ventromedial
A:Reference number: PC4034; MUID:95314614; PMID:7794258
A:Accession: PC4034
A:Molecule type: mRNA
A:Residues: 1-167 <FUN>
A:Cross-references: UNIPROT:P50596
A:Experimental source: adipose tissue
A>Note: The authors translated the codon AAA for residue 32 as Thr
R:Murakami, T.; Shima, K.
Biochem. Biophys. Res. Commun. 209, 944-952, 1995
A:Title: Cloning of rat obese cDNA and its expression in obese rats.
A:Reference number: JC4142; MUID:95251725; PMID:7733988
A:Accession: JC4142
A>Status: preliminary
A:Molecule type: mRNA
A:Residues: 1-167 <MUR>
A:Cross-references: DDBJ:D49653; NID:g995614; PIDN:BAA08529.1; PID:g995615
A:Experimental source: liver
A:Comment: This protein is proposed to function as part of a signalling pathway from ad
C:Genetics:
A:Gene: obese
C:Superfamily: leptin
C:Keywords: adipose tissue
F:1-21/Domain: signal sequence #status predicted <SIG>
F:22-167/Product: leptin #status predicted <MAT>

Query Match 82.2%; Score 605; DB 1; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.3e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVARQRTVGLDFIPGLHPILTLTKMDQTLAV 81
QY 61 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 120
DB 82 YQOILTSPSRNVIQISNDLENLRLDLHLVAFSKSCHLPWASGLETLSLGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 5
I55622
rat Ob - rat
C:Species: Rattus sp. (rat)
C>Date: 26-Jul-1996 #sequence_revision 26-Jul-1996 #text_change 16-Jul-1999
C:Accession: I55622
R:Ogawa, Y.; Masuzaki, H.; Isse, N.; Okazaki, T.; Mori, K.; Shigemoto, M.; Satoh, N.; Ta
J. Clin. Invest. 96, 1647-1652, 1995
A:Title: Molecular cloning of rat obese cDNA and augmented gene expression in geneticall
```

A:Reference number: I55622; MUID:95386724; PMID:7657834
A:Accession: I55622
A>Status: preliminary; translated from GB/EMBL/DBJ
A:Molecule type: mRNA
A:Residues: 1-167 <RES>
A:Cross-references: GB:D45862; NID:g1018990; PIDN:BAA08296.1; PID:g1018991
C:Superfamily: lepton

Query Match 82.2%; Score 605; DB 2; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.3e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
DB 22 VPIHKQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81

QY 61 YQOILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLTDLISLGGVLEASGY 120
DB 82 YQOILTSMPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLTDLISLGGVLEASGY 141

QY 121 TEVVALSRLOGLSLODMLWQIDLSGPC 146
DB 142 TEVVALSRLOGLSLODMLWQIDLSGPC 167

RESULT 6
AB3281
glutamate dehydrogenase (EC 1.4.1.2) [imported] - Brucella melitensis (strain 16M)
C:Species: Brucella melitensis
C>Date: 01-Feb-2002 #sequence_revision 01-Feb-2002 #text_change 09-Jul-2004
C:Accession: AB3281
R:DelVecchio, V.G.; Kaputal, V.; Redkar, R.J.; Patra, G.; Mujar, C.; Los, T.; Ivanova,
.; Mazur, M.; Goldsman, E.; Seikov, E.; Elzer, P.H.; Hagius, S.; O'Callaghan, D.; Letess
Proc. Natl. Acad. Sci. U.S.A. 99, 443-448, 2002
A:Title: The genome sequence of the facultative intracellular pathogen Brucella melitensis
A:Reference number: AD3252; PMID:11756688
A:Accession: AB3281
A>Status: preliminary
A:Molecule type: DNA
A:Residues: 1-1600 <KUR>
A:Cross-references: UNIPROT:Q8YJ55; GB:AE008917; PIDN:AAL51413.1; PID:g17982118; GSPDB:G
A:Experimental source: strain 16M
C:Genetics:
A:Gene: BMEI0231
A:Map position: 1
C:Keywords: oxidoreductase

Query Match 11.1%; Score 81.5; DB 2; Length 1600;
Best Local Similarity 24.6%; Pred. No. 55;
Matches 32; Conservative 23; Mismatches 52; Indels 23; Gaps 5;

QY 6 VQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVYQOIL 65
DB 97 VNDNMPFLDLSINGELND--HTSQI-----FMVHPVLDIRKDELVLILGEAS 143

QY 66 TSPSPNRNVIQISNDLENLRLDHLVAFSKSCHLPWASGLTDLISLGGVLEASGYTEVVA 125
DB 144 QLAPAKGVERVS-----LVQIHLPAKQAKADLTAGLRV--LQGV--RSAVSDWKPM 193

QY 126 LSRLOGLSLOD 135
DB 194 LKRLDGAIDD 203

RESULT 7
S54039
hypothetical protein YDR055w - yeast (Saccharomyces cerevisiae)
N:Alternate names: hypothetical protein D4214; hypothetical protein YBRB444; hypothetical
C:Species: Saccharomyces cerevisiae
C>Date: 08-Jul-1995 #sequence_revision 01-Sep-1995 #text_change 09-Jul-2004
C:Accession: S54039; S58835; S61744; S67871
R:Hunt, S.; Bowman, S.; Harris, D.
submitted to the EMBL Data Library, May 1995

A:Reference number: S54031
A:Accession: S54039
A:Molecule type: DNA
A:Residues: 1-444 <HUN>
A:Cross-references: UNIPROT:Q12355; EMBL:Z49209; NID:g798897; PIDN:CAA89084.1; PID:g798
R:Brandt, P.; Otto, B.; Ramlow, S.; Blocker, H.
submitted to the EMBL Data Library, January 1995
A:Reference number: S58832
A:Accession: S58835
A:Molecule type: DNA
A:Residues: 1-444 <BRA>
R:Brandt, P.; Ramlow, S.; Otto, B.; Blocker, H.
Yeast 12, 85-90, 1996
A:Title: Nucleotide sequence analysis of a 32,500 bp region of the right arm of Sacchar
A:Reference number: S61741; MUID:96381250; PMID:8789263
A:Accession: S61744
A:Molecule type: DNA
A:Status: nucleic acid sequence not shown; translation not shown
A:Residues: 1-444 <BRW>
A:Cross-references: EMBL:X84162; NID:g706817; PIDN:CAA58971.1; PID:g706821
R:Brandt, P.; Ramlow, S.; Otto, B.; Blocker, H.
submitted to the EMBL Data Library, January 1995
A:Reference number: S67587
A:Accession: S67871
A:Molecule type: DNA
A:Residues: 1-444 <BLO>
A:Cross-references: EMBL:Z74351; NID:g1431498; PIDN:CAA98873.1; PID:g1431499; MIPS:YDR0
A:Experimental source: strain S288C
C:Genetics:
A:Gene: SCD:PST1
A:Cross-references: SGD:S0002462
A:Map position: 4R
C:Keywords: transmembrane protein
F:5-2/Domain: transmembrane #status predicted <TMM>

Query Match 10.9%; Score 80.5; DB 2; Length 444;
Best Local Similarity 24.3%; Pred. No. 13;
Matches 35; Conservative 23; Mismatches 49; Indels 37; Gaps 6;

QY 2 PIQKQDDTKLIKIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAVYQOIL 48
DB 181 PVETVSDLSQFSGFNQTKITFDLWANNISLUTDVHVSFANLQKINSLSLGINNIS 240

QY 49 LTLKMD---QTLAVYQOILTSMPSPNRNVIQISND-----LENLRLDHLVAFSKSCHLP 99
DB 241 LNFTKLNTIGQTFSI-----VENDYLNKLSFNSLSTIGGALVVAANTGLQ 285

QY 100 WASGLETLDSLGGVLEASGYSTEV 123
DB 286 KIGGLDNLTTIGTGLEVVGNFTSL 309

RESULT 8
T01362
probable myosin heavy chain At2g34730 - Arabidopsis thaliana
N:Alternate names: hypothetical protein T29F13.6
C:Species: Arabidopsis thaliana (mouse-ear cress)
C>Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 09-Jul-2004
C:Accession: T01362; C84760
R:Rounsley, S.D.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Sykes, S.M.; Kau
submitted to the EMBL Data Library, May 1998
A:Description: Arabidopsis thaliana chromosome II BAC T29F13 genomic sequence.
A:Reference number: Z14179
A:Accession: T01362
A>Status: translated from GB/EMBL/DBJ
A:Molecule type: DNA
A:Residues: 1-829 <ROU>
A:Cross-references: UNIPROT:O64584; EMBL:AC003096; NID:g3132469; PID:g3132472
A:Experimental source: cultivar Columbia
R:Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.L.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.

euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
 Nature 402, 761-768, 1999
 A>Title: Sequence and analysis of chromosome 2 of the plant *Arabidopsis thaliana*.
 A;Reference number: A84420; MUID:20083487; PMID:10617197
 A;Accession: C84760
 A;Status: preliminary
 A;Molecule type: DNA
 A;Residues: 1-829 <STO>
 A;Cross-references: GB:AE002093; NID:g3132472; PIDN:AAC16261.1; GSPDB:GN00139
 C;Genetics:
 A;Gene: At2g34730; T29F13.6
 A;Map position: 2
 A;Introns: 728/2; 770/3

```

Query Match      10.7%; Score 79; DB 2; Length 829;
Best Local Similarity 21.5%; Pred. No. 40;
Matches 34; Conservative 27; Mismatches 45; Indels 52; Gaps 6

Qy 3 IQKVDDTKLIKIVTRINDISHTQSVSKQVGTGLDFIPLGLHPILTLKXMDQFLAVY- 61
| : : : | : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 57 ISRVSD--SIIRGMVTAIES-----DAAEKIAQKD-----LELSKIRETLTLLYH 99

Qy 62 -----QQILTMPERNVIOIQNDELRLDLHLVAFKSKSLHP 99
| : : : | : : | : : | : : | : : | : : | : : | : : | : : | : : |
Db 100 VGSENESSSRLLHDELTQSSSSKKKAKOLLMLVEELTNREYTHIN----- 150

```

Qy 100 WASGLETLDLSGLVLEASGYSTEWALSRLOGSLODML 137
||| ||| : : : : :
|| | : : : : :
Dd 151 - GSGATVDLSL--LDSSPHETRSKTVDKMDLSKSIL 185

RESULT 9
H84583
hypothetical protein At2g20010 [imported] - Arabidopsis thaliana
C/Species: Arabidopsis thaliana (mouse-ear cress)
C/Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C/Accession: H84583
R/Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
Muss, D.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.
Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.C.; Nierman, W.C.; White, O.

A>Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A/Reference number: A84420; MUID:20083487; PMID:10617197
A/Accession: H84583
A>Status: preliminary
A/Molecule type: DNA
A/Residues: 1-952 <STO>
A/Cross-references: UNIPROT:Q9SL80; GB:AE002093; NID:g4580471; PIDN:AAD24395.1; GSPDB:GN
C/Genetic:
A/Gene: At2g20010
A/Map position: 2

```

Query Match      10.7%; Score 79; DB 2; Length 952;
Best Local Similarity 33.3%; Pred.No. 48;
Matches 23; Conservative 15; Mismatches 19; Indels 12; Gaps 3;

QY   45 LHPILTLSKMDQTALVYQQILTSMPSSR~NVIQISNDLENLRLHLLVLAF-----SK 94
      :|||:::|||||:|||||:|||||:|||||:|||||:|||||:|||||:
Db    186 LYPCVPLSKSDKSVQOOLKIIRSGLEPLDTGKTGETONLRSLVWGLASRONNNIGSE 245
```

Qy	95	SCHLPWASG	103
		:	:
Db	246	TCH--WADG	252

RESULT 10
S75514
sensory transduction histidine kinase slr1324 - *Synechocystis* sp. (strain PCC 6803)
N:Alternate names: protein slr1324
C:Species: *Synechocystis* sp.
A:Variety: PCC 6803
C:Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
C:Accession: S75514

R; Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.
O, K.; Okumura, S.; Shimpo, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasud.
DNA Res. 3, 109-136, 1996
A; Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis*
s.
A; Reference number: S74322; MUID:97061201; PMID:8905231
A; Accession: S7514
A; Status: nucleic acid sequence not shown; translation not shown
A; Molecule type: DNA
A; Residues: 1-420 <KAN>
A; Cross-references: UNIPROT:P74004; EMBL:D90911; GB:AB001339; NID:G1653083; PIDN:EAA180.
A; Note: The nucleotide sequence was submitted to the EMBL Data Library. June 1996

A;Start codon: GTG
 C;Superfamily: sensory transduction system regulatory protein; response regulator homologs, heterodimeric
 C;Keywords: phosphoprotein
 F;33-146/Domain: response regulator homology <RRH>
 F;85/Binding site: phosphate (Asp1, conserved)
 F;status: predicted

Query Match	10.6%;	Score 78;	DB 2;	Length 420;
Best Local Similarity	28.2%;	Pred. No. 21;		
Matches	33;	Conservative	19;	Mismatches 44; Indels 22; Gaps 5;
Qy	43	PGUHPILTISKMDQTILA---VYQQILTSPSRNVIQISNDLENLRDLHLVLAFSK-----	94	
		: : : : : :		
Dd	29	PRLHILL----IEDNLAEARLLGSLKSGPKENF--AFNHVQRIGDALTVLAQGEKFDDI	82	
		: : : : : :		
Qy	95	--SCHLPWASGLSETLSLGG-----VLEASGYSTEVVALSRLGGSLODMLMQLDLS	143	
		: : : : : :		
Dd	83	LLEDLTIPDSOGINSLPKIOSHPONLPTIVLTHYODEELALEAVROGAODYLVKRVDVS	139	
		: : : : : :		

```

RESULT 11
AI0055
probable soluble lytic murein transglycosylase (EC 3.2.1.-) [imported] - Yersinia pestis
C:Species: Yersinia pestis
C:Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C:Accession: AI0055
R:Farhalla, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B
deno-farriga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.;
il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell,
Nature 413, 523-527, 2001
A::title: Genome sequence of Yersinia pestis, the causative agent of plague.
A::Reference number: AB0001: PMID:21470413: PMID:11586360

```

A;Accession: A10035
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-639 <KUR>
A;Cross-references: UNIPROT:Q8Z1P2; GB:AL590842; PIDN:CAC89308.1; PID:GI5978544; GSPDB:G
C;Gene: YPO452
C;Superfamily: soluble lytic transglycosylase
C;Keywords: glycosidase; hydrolase

Query Match	10.6%;	Score 78;	DB 2;	Length 639;
Best Local Similarity	23.0%;	Pred.No.35;		
Matches	32;	Conservative	21;	Mismatches 38; Indels 48; Gaps 5;
QY	27	TQSVSSKQKVTGLDFTIPGLHPILTLKSKMDOTLAVYQQILTSMPSRNVIQISNDLENLRDL	86	
Db	69	TQDLSQVSTAQVKDFL-NRHPTLPAPK-----SLFSRFV-----NELARREDW	110	
QY	87	LHVLAFSKSHLP-----WASGLETL-----DSLGGVLEA	116	
Db	111	RGLLTSPAPRVAARCNYVYAKWATGQSVAWEGASEIWLNGQSLPGCKDKLFSVWQQ	170	
QY	117	SGYSTEVVALSRLOQSLQD	135	
Db	171	AGHOTPLATLARMKLAKE	189	

RESULT 12
B42374

phosphotransferase system enzyme I (EC 2.7.3.9) - *Staphylococcus carnosus*
C/Species: *Staphylococcus carnosus*
C/Date: 10-Jul-1992 #sequence_revision 31-Jan-1997 #text_change 09-Jul-2004
C/Accession: B42374; S17075
R/Kohlbrecher, D.; Eisermann, R.; Hengstenberg, W.
J. Bacteriol. 174, 2208-2214, 1992
A/Title: *Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system: molecular studies of the gene product.*
A/Reference number: A42374; MUID:92202148; PMID:1551842
A/Accession: B42374
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-574 <KOH>
A/Cross-references: UNIPROT:P23533; GB:M69050; NID:G153073; PIDN:AAA26664.1; PID:G153075
R/Eisermann, R.; Fischer, R.; Kessler, U.; Neubauer, A.; Hengstenberg, W.
Eur. J. Biochem. 197, 9-14, 1991
A/Title: *Staphylococcal phosphoenolpyruvate-dependent phosphotransferase system. Purification and sequencing of the pteH gene.*
A/Reference number: S15367; MUID:91200066; PMID:1901791
A/Accession: S17075
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-90 <EIS>
A/Cross-references: EMBL:X60766; NID:G46907; PIDN:CAA43176.1; PID:G46909
C/Superfamily: phosphotransferase system enzyme I; phosphotransferase system enzyme I hc
C/Keywords: phosphoprotein; phosphotransferase; sugar transport system
F:5-563/Domain: phosphotransferase system enzyme I homology <PT1>

Query Match 10.5%; Score 77.5; DB 1; Length 574;
Best Local Similarity 25.0%; Pred. No. 34;
Matches 32; Conservative 27; Mismatches 54; Indels 15; Gaps 5;

QY 11 KTLIKITVTR--INDISHTQSVSSKKVTCGLDFIPGLHPILTLTKMDQTLAVVQQILTS 67
DB 188 RTHSAIMSRSLPEPAVGVTKSIEEVEAGDTIVDGMTGDLINPSDEVIAEYQE---- 243
QY 68 MPRSNVTQISNDLENRDLHLVAFSKSCHLPWASGLFETLDSIGGVLE--ASG---YSTE 122
DB 244 -KRENFPPKQELQKLQDASVTA--DGHHVELAANIGTPNDLPVGIENGAGGIGLYRTE 300
QY 123 VVALSRQLQ 130
DB 301 FLYMGDRQ 308

RESULT 13
S77486
ribosomal protein S5 - *Synechocystis* sp. (strain PCC 6803)
N/Alternate names: protein sll1812
C/Species: *Synechocystis* sp.
A/Variety: PCC 6803
C/Date: 25-Apr-1997 #sequence_revision 25-Apr-1997 #text_change 09-Jul-2004
R/Kaneko, T.; Sato, S.; Kotani, H.; Tanaka, A.; Asamizu, E.; Nakamura, Y.; Miyajima, N.; O, K.; Okumura, S.; Shimpou, S.; Takeuchi, C.; Wada, T.; Watanabe, A.; Yamada, M.; Yasuda DNA Res. 3, 109-136, 1996
A/Title: Sequence analysis of the genome of the unicellular cyanobacterium *Synechocystis* sp.
A/Reference number: S74322; MUID:97061201; PMID:8905231
A/Accession: S77486
A/Status: nucleic acid sequence not shown; translation not shown
A/Molecule type: DNA
A/Residues: 1-173 <KAN>
A/Cross-references: UNIPROT:P73304; EMBL:D90905; GB:AB001339; NID:G1652360; PIDN:BAA1733
C/Note: the nucleotide sequence was submitted to the EMBL Data Library, June 1996
C/Genetics:
A/Gene: rps5
C/Superfamily: ribosomal protein S5/S2
C/Keywords: protein biosynthesis; ribosome

Query Match 10.4%; Score 76.5; DB 2; Length 173;
Best Local Similarity 31.2%; Pred. No. 9.2;
Matches 29; Conservative 12; Mismatches 41; Indels 11; Gaps 3;

Qy	6	VODDTKLITVIRINDISH-TOSVSSKQKVGLDFIPG-----LHPILTILSKMDQ 56
Db	70	VADGKKQLIEVPLTKNSIITHITNGVSGGAKVVRPAAPGTVIAGGAVRTVZELAGVKN 129
Qy	57	TLAVYQQLTSPMSPRNVIQISNDLENRLDLHV 89
Db	130	ILA--KOLGSPNPLNNARAAINALETITFTFSEV 160

RESULT 14

A83967
carbamoyl-phosphate synthetase (glutaminase subunit) pyrAA [imported] - Bacillus
C/Species: Bacillus halodurans
C/Date: 01-Dec-2000 #accession_change 09-Jul-2004
C/Accession: A83967
R/Takami, H.; Nakasone, K.; Takaki, Y.; Maeno, G.; Sasaki, R.; Masui, N.; Fujii,
Nucleic Acids Res. 28, 4317-4331, 2000
A/Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans
A/Reference number: A83650; MUID:20512582; PMID:11058132
A/Accession: A83967
A/Status: preliminary
A/Molecule type: DNA
A/Residues: 1-362 <STO>
A/Cross-references: UNIPROT:Q9K9V8; GB:AP001515; GB:EA000004; NID:G10174886; P
A/Experimental source: strain C-125
C/Genetics:
A/Gene: pyrAA
C/Superfamily: carbamoyl-phosphate synthase (glutamine-hydrolyzing) small chain

Query Match	10.4%;	Score 76.5;	DB 2;	Length 362;
Best Local Similarity	31.0%;	Pred. No. 24;		

Qy	78	NDLENRLDLHLVLAFLSKCHLP--WASGLETLDSLGGVLEASCYS-----TEVVALSRLQGL	131
Db	66	DDFESMNPATHLGLVAKEDIPSNWRSE-ESLDSLLKAKQIPGLSGIDTRKLTLLRMHG	124
Qy	132	SLQDMLWQLDL	142
Db	125	TLKGQLCPLDV	135

RESULT 15

E86305
Probable trehalose-6-phosphate synthase [imported] - Arabidopsis thaliana
C:Species: Arabidopsis thaliana (mouse-ear cress)
C:Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
C:Accession: E86305
R:Theologian, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.
Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.;
ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 2000
A:Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.
C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.;
Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A:Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.
ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A:Title: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A:Reference number: A86141; MUID:21016719; PMID:11130712
A:Accession: E86305
A:Status: Preliminary
A:Molecule type: DNA
A:Residues: 1-822 <STO>
A:Cross-references: UNIPROT:Q9F5Z7; GB:AE005172; NID:g9802765; PIDN:AAF99834.1
C:Genetics:
A:Map position: 1

Query Match 10.4%; Score 76.5; DB 2; Length 822;
Best Local Similarity 31.6%; Pred. No. 67;
Matches 31; Conservative 16; Mismatches 36; Indels 15; Gaps 4;
Qv 38 GLDFIPGLHPILTILTSKNDQTLAVVQQILTSWPSNRVTQISNDLENRLDLHLVAFPSKCH 97

Db 470 GLDFMSELNGIIPESQM-----RKIPQLPEQDVIOQYSQNN---ELIILGFFGTIA 521
Qy 98 LPWASGLETD-----SLGGVLEA--SGYSTEVVALSR 128
Db 522 EPMNSGKEMDLKLNPELKGTLKALCNDPKTTVVVLSR 559

Search completed: March 12, 2005, 05:04:36
Job time : 23.8562 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:44:37 ; Search time 105.419 Seconds
(without alignments)
709.207 Million cell updates/sec

Title: US-10-049-182-6
Perfect score: 736
Sequence: 1 VPIQKVDYTKLTIKIVTR.....SRLOSLQDMLWQLDLSPEC 146

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Uniprot_03: *
1: uniprot_prot: *
2: uniprot_trembl: *

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	736	100.0	167	1 OB_HUMAN	P41159 homo sapien
2	736	100.0	167	2 Q6NT58	Q6NT58 homo sapien
3	733	99.6	146	1 OB_PANTR	O02750 pan troglod
4	728	98.9	146	1 OB_GORGO	Q95189 gorilla gor
5	721	98.0	146	1 OB_PONPY	Q95234 pongo pygma
6	721	98.0	146	1 OB_PONPY	Q28504 macaca mula
7	639	86.8	167	1 OB_FELCA	Q9N2C1 felis silve
8	628	85.3	146	2 Q6TBR8	Q6TBR8 bubalus bub
9	628	85.3	167	1 OB_BOVIN	P50595 bos taurus
10	627	85.2	167	1 OB_PIG	Q29406 sus scrofa
11	624	84.8	146	1 OB_SHERP	Q28603 ovis aries
12	619	84.1	167	1 OB_MOUSE	P41160 mus musculus
13	605	82.2	167	1 OB_RAT	P50596 rattus norv
14	586.5	79.7	163	1 OB_CANFA	O02720 canis famil
15	576.5	78.3	145	1 OB_CHICK	O42164 gallus gall
16	576.5	78.3	145	1 OB_MELGA	Q93416 meleagris g
17	522.5	71.0	145	2 Q6S9B2	Q6S9B2 equus cabal
18	505	68.6	167	1 OB_SMICR	Q9XW9 sminthopsis
19	498	67.7	119	2 Q861R2	Q861R2 bubalus bub
20	477	64.8	118	2 Q8MK60	Q8MK60 alopec lago
21	476	64.7	118	2 Q8MK58	Q8MK58 vulpes vulp
22	474	64.4	118	2 Q8MK59	Q8MK59 nyctereutes
23	469	63.7	118	2 Q8MK61	Q8MK61 canis famil
24	465	63.2	167	2 Q706D0	Q706D0 halichoerus
25	463	62.9	167	2 Q706D1	Q706D1 phoca vitul
26	462	62.8	123	2 Q95KW9	Q95KW9 myotis luci
27	449	61.0	109	2 Q866S7	Q866S7 bubalus bub
28	447	60.7	99	1 OB_HORSE	Q9TU09 equus cabal
29	439	59.6	109	2 Q864V1	Q864V1 camelus dro
30	387	52.6	106	2 Q95MG5	Q95MG5 capra hircu
31	380	51.6	90	2 Q8WMK7	Q8WMK7 delphinapte

32	376	51.1	90	2 Q7TMN2	Q7tmn2 marmota mon
33	375	51.0	90	2 Q7TMN0	Q7tmn0 tamiasciuru
34	371	50.4	91	2 Q7YR78	Q7yr78 bubalus bub
35	368	50.0	90	2 Q8WML2	Q8wml2 oryctolagus
36	367	49.9	90	2 Q8WML1	Q8wml1 chaetophrac
37	367	49.9	90	2 Q7YQJ8	Q7yqj8 vulpes vulp
38	361	49.0	89	2 Q8WML0	Q8wml0 nephtitis me
39	361	49.0	89	2 Q6YIR1	Q6yir1 ursus ameri
40	353	48.0	89	2 Q8WMK9	Q8wmk9 procyon lot
41	342	46.5	90	2 Q8WMK8	Q8wmk8 eptesicus f
42	340	46.2	86	2 Q8WJ10	Q8wj10 bos taurus
43	339.5	46.1	100	2 Q8UWJ3	Q8uwj3 gallus gall
44	330	44.8	90	2 Q7TMN1	Q7tmn1 castor cana
45	195	26.5	42	2 Q6QLP9	Q6qlp9 bos indicus

ALIGNMENTS

RESULT 1					
ID	OB_HUMAN	STANDARD;	PRT;	167 AA.	
AC	P41159; O15158;				
DT	01-FEB-1995 (Rel. 31, Created)				
DT	01-FEB-1995 (Rel. 31, Last sequence update)				
DT	25-OCT-2004 (Rel. 45, Last annotation update)				
DE	Leptin precursor (Obesity factor) (Obese protein).				
GN	Name=LEP; Synonyms=OB;				
OS	Homo sapiens (Human).				
OC	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;				
OC	Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.				
OX	NCBI_TaxID=9606;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;				
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;				
RT	"Positional cloning of the mouse obese gene and its human homologue.";				
RL	Nature 372:425-432(1994).				
RN	[2]				
RP	ERRATUM.				
RA	Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;				
RL	Nature 374:479-479(1995).				
RN	[3]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=95309556; PubMed=7789654;				
RA	Masuzaki H., Ogawa Y., Isse N., Satoh N., Okazaki T., Shigemoto M.,				
RA	Mori K., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,				
RA	Nakao K.;				
RT	"Human obese gene expression. Adipocyte-specific expression and				
RT	regional differences in the adipose tissue.";				
RL	Diabetes 44:855-858(1995).				
RN	[4]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96223958; PubMed=8626726; DOI=10.1074/jbc.271.8.3971;				
RA	Gong D.W., Bi S., Pratley R.E., Weintraub B.D.;				
RT	"Genomic structure and promoter analysis of the human obese gene.";				
RL	J. Biol. Chem. 271:3971-3974(1996).				
RN	[5]				
RP	SEQUENCE FROM N.A.				
RA	Chehab F.F., Lim M.E.;				
RL	Submitted (DEC-1995) to the EMBL/GenBank/DBJ databases.				
RN	[6]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96070903; PubMed=7499240; DOI=10.1074/jbc.270.46.27728;				
RA	Isse N., Ogawa Y., Tamura N., Masuzaki H., Mori K., Okazaki T.,				
RA	Satoh N., Shigemoto M., Yoshimasa Y., Nishi S., Hosada K., Inazawa J.,				
RA	Nakao K.;				
RT	"Structural organization and chromosomal assignment of the human obese				
RT	gene.";				
RL	J. Biol. Chem. 270:27728-27733(1995).				
RN	[7]				
RP	SEQUENCE FROM N.A.				
RX	MEDLINE=96198511; PubMed=8621021;				

RA Niki T., Mori H., Tamori Y., Kishimoto-Hashimoto M., Ueno H.,
RA Araki S., Masugi J., Sawant N., Majithia H.R., Rais N.,
RA Hashimoto M., Taniguchi H., Kasuga M.,
RT "Human obese gene: molecular screening in Japanese and Asian Indian
RL NIDDM patients associated with obesity.",
RN Diabetes 45:675-678(1996).
RP SEQUENCE FROM N.A.
RA Lu L., Fu Z., Xu M., Fu Y., Hu Z.,
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN SEQUENCE FROM N.A.
RP TISSUE=Placenta;
RC MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RX Strausberg R.L., Feingold E.A., Grouse L.H., Dege J.G.,
RA Klausner R.D., Collins F.S., Wagner K.H., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zebberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M.J., Soares M.B., Bonaldo M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalón D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M.,
RA Butterfield Y.S., Krzywinski M.I., Skalska U., Smalilus D.E.,
RA Schnerch A., Schein J.E., Jones S.J.M., Marra M.A.,
RT "Generation and initial analysis of more than 15,000 full-length human
RN and mouse cDNA sequences.",
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [10]
RP INTERACTION WITH SIGLEC6.
RX MEDLINE=99357812; PubMed=10428856; DOI=10.1074/jbc.274.32.22729;
RA Patel N., Brinkman-Van der Linden E.C.M., Altman S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.,
RT "OB-RP1/Siglec-6: A leptin- and sialic acid-binding protein of the
RN immunoglobulin superfamily.",
RL J. Biol. Chem. 274:22729-22738(1999).
RN [11]
RP ERRATUM.
RA Patel N., Brinkman-Van der Linden E.C.M., Altman S.W., Gish K.C.,
RA Balasubramanian S., Timans J.C., Peterson D., Bell M.P., Bazan J.F.,
RA Varki A., Kastelein R.A.,
RL J. Biol. Chem. 274:28058-28058(1999).
RN [12]
RP STRUCTURE BY NMR.
RX MEDLINE=97309492; PubMed=9166907; DOI=10.1016/S0014-5793(97)00353-0;
RA Kline A.D., Becker G.W., Churgay L.M., Landen B.E., Martin D.K.,
RA Muth W.L., Rathnachalam R., Richardson J.M., Schoner B., Ulmer M.,
RA Hale J.B.,
RT "Leptin is a four-helix bundle: secondary structure by NMR.",
RN FEBS Lett. 407:239-242(1997).
RN [13]
RP X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS).
RX MEDLINE=97289390; PubMed=9144295;
RA Zhang F., Basinski M.B., Beals J.M., Briggs S.L., Churgay L.M.,
RA Clawson D.K., Dimarchi R.D., Furman T.C., Hale J.E., Heising H.M.,
RA Schoner B.E., Smith D.P., Zhang X.Y., Wery J.P., Schevitz R.W.,
RT "Crystal structure of the obese protein leptin-B100.",
RN Nature 387:206-209(1997).
RN [14]
RP VARIANT MET-94.
RA Bartholomew D.W., Mclellan J.M.,
RT "A novel polymorphism in the leptin gene.",
RN Hum. Mutat. 12:220-220(1998).
RN [15]
RP VARIANT MORBID OBESITY TEP-105.
RX MEDLINE=98160176; PubMed=9500540;

RA Strobel A., Issad T., Camoin L., Ozata M., Strosberg A.D.,
RT "A leptin missense mutation associated with hypogonadism and morbid
RN obesity.",
RL Nat. Genet. 18:213-215(1998).
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBUNIT: Interacts with SIGLEC6.
CC -!- SUBCELLULAR LOCATION: Secreted.
CC -!- DISEASE: Defects in LEP may be a cause of autosomal recessive
CC obesity [MIM:601665].
CC -!- SIMILARITY: Belongs to the leptin family.
CC -!- DATABAS: NAME=RAID Systems' cytokine mini-reviews: LEP;
CC WWW="http://www.rndsystems.com/asp/g_sitebuilder.asp?bodyId=213".
CC -----
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CC -----
DR EMBL; U18915; AAA60470.1; -;
DR EMBL; D49487; BAA08448.1; -;
DR EMBL; U43653; AAC50400.1; -;
DR EMBL; U43415; AAC31860.1; -;
DR EMBL; D63710; BAA09839.1; -;
DR EMBL; D63709; BAA09839.1; JOINED..
DR EMBL; D63519; BAA09787.1; -;
DR EMBL; D63518; BAA09787.1; JOINED.
DR EMBL; AF008123; AAB63507.1; -;
DR EMBL; BC080830; AAB60830.1; -;
DR PIR; A38952; LTHU.
DR PIR; I53166; I53166.
DR PDB; 1AX8; X-ray; @=22-167.
DR Genew; HGNC:6553; LEP.
DR MIM; 164160; -;
DR MIM; 601665; -;
DR GO; GO:0005615; C:extracellular space; TAS.
DR GO; GO:0006112; P:energy reserve metabolism; TAS.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
DR 3D-structure; Diabetes mellitus; Disease mutation; Obesity;
DR Polymorphism; Signal.
KW SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167
FT VARIANT 49 49 Missing (in 30% the clones).
FT VARIANT 94 94 /FTID=VAR_004196.
FT VARIANT 105 105 /FTID=VAR_004197.
FT VARIANT 110 110 R -> W (in morbid obesity and
FT VARIANT 110 110 hypogonadism).
FT VARIANT 110 110 /FTID=VAR_008094.
FT VARIANT 110 110 V -> M (in dbSNP:1800564).
FT VARIANT 110 110 /FTID=VAR_011955.
FT VARIANT 110 110 Q -> R (in Ref. 8).
FT CONFLICT 96 96
FT HELIX 25 44
FT HELIX 72 87
FT TURN 88 88
FT TURN 92 114
FT TURN 115 116
FT HELIX 128 131
FT HELIX 132 135
FT STRAND 137 137
FT TURN 138 139
FT STRAND 140 140

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Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146

RESULT 4
OB GORGO
ID OB GORGO STANDARD; PRT; 146 AA.
AC Q95189;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Gorilla gorilla gorilla (Lowland gorilla).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Gorilla.
OX NCBI_TaxID=9595;
RN [1]
RP SEQUENCE FROM N.A.
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (OCT-1996) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC
CC EMBL; U72873; AAB17091.1; -
CC HSP; P41159; IAX8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity.
CC DISULFID 96 146 By similarity.
CC SEQUENCE 146 AA; 16031 MW; 02C43BF6B9A4C85C CRC64;

Query Match 98.9%; Score 728; DB 1; Length 146;
Best Local Similarity 98.6%; Pred. No. 5e-59;
Matches 144; Conservative 2; Mismatches 0; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
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RESULT 5
OB PONPY
ID OB PONPY STANDARD; PRT; 146 AA.
AC Q95234;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pongo pygmaeus (Orangutan).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pongo.
OX NCBI_TaxID=9600;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostek P.R.;
RT "Cloning of obese genes from different species: a comparison of the
RT gene structures and the sequences of the obese gene products,
RT leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC or send an email to license@isb-sib.ch).
CC
CC EMBL; U72873; AAB17092.1; -
CC HSP; P41159; IAX8.
CC InterPro; IPR009079; 4_helix_cytokine.
CC InterPro; IPR000065; Leptin.
CC Pfam; PF02024; Leptin; 1.
CC PRINTS; PR00495; LEPTIN.
CC ProDom; PD005698; Leptin; 1.
CC Obesity.
CC DISULFID 96 146 By similarity.
CC SEQUENCE 146 AA; 16195 MW; 3F50A13338FDBD4 CRC64;

Query Match 98.0%; Score 721; DB 1; Length 146;
Best Local Similarity 97.3%; Pred. No. 2.2e-58;
Matches 142; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

Qy 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Db 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
Qy 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Db 61 YQQLITSPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGLVLEASGYS 120
Qy 121 TEVALSRLOGLSQDMLWQLDLSGPC 146
Db 121 TEVALSRLOGLSQDMLWQLDLSGPC 146

RESULT 6
OB MACMU
ID OB MACMU STANDARD; PRT; 167 AA.
AC Q28504;
DT 01-NOV-1997 (Rel. 35, Created)
DT 01-NOV-1997 (Rel. 35, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
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FT HELIX 142 160
FT HELIX 161 163

Query Match 100.0%; Score 736; DB 1; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||
DB 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
|||

QY 61 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
|||
DB 82 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
|||

QY 121 TEWVALSRLOGLQDMLWQDLSPGC 146
|||
DB 142 TEWVALSRLOGLQDMLWQDLSPGC 167
|||

RESULT 2

OB PANTR PRELIMINARY; PRT; 167 AA.

AC Q6NT58
DT 05-JUL-2004 (Tremblrel. 27, Created)
DT 05-JUL-2004 (Tremblrel. 27, Last sequence update)
DT 05-JUL-2004 (Tremblrel. 27, Last annotation update)
DE Leptin.
GN Name=LEP;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RX MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;
RA Strausberg R.L., Feingold E.A., Grouse L.H., Derge J.G.,
RA Klausner R.D., Collins F.S., Wagner L., Shenmen C.M., Schuler G.D.,
RA Altschul S.F., Zeeberg B., Buetow K.H., Schaefer C.F., Bhat N.K.,
RA Hopkins R.F., Jordan H., Moore T., Max S.I., Wang J., Hsieh F.,
RA Diatchenko L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,
RA Stapleton M., Soares M.B., Donald M.F., Casavant T.L., Scheetz T.E.,
RA Brownstein M.J., Udén T.B., Toshiyuki S., Carninci P., Prange C.,
RA Raha S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J.,
RA Boeak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H.,
RA Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W.,
RA Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A.,
RA Fahey J., Helton E., Kettman M., Madan A., Rodrigues S., Sanchez A.,
RA Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G.,
RA Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C.,
RA Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.,
RA Krzywinski M.I., Skalska U., Smallos D.E., Schnerch A., Schein J.E.,
RA Jones S.J., Marra M.A.;
RT "Generation and initial analysis of more than 15,000 full-length human
and mouse cDNA sequences."
RL Proc. Natl. Acad. Sci. U.S.A. 99:16899-16903(2002).
RN [2]

RP SEQUENCE FROM N.A.
RC TISSUE=PCR rescued clones;
RA Strausberg R.;
RL Submitted (APR-2004) to the EMBL/GenBank/DBJ databases.
DR EMBL; BC069323; AAH69323.1; -;
DR HSP; P41159; 1AX8.
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR009079; 4 helix cytokine.
DR Pfam; PF02024; LEPTIN.
DR InterPro; IPR00065; Leptin.
DR PRINTS; PR00495; LEPTIN.
DR PRODom; PD005698; Leptin; 1.
DR PRODom; PD005698; Leptin; 1.
SQ SEQUENCE 167 AA; 18612 MW; BE1A046FFB1554DE CRC64;

Query Match 100.0%; Score 736; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 1.1e-59;
Matches 146; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||
DB 22 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 81
|||

QY 61 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 120
|||
DB 82 YQOILTSMPSRNVIQISNDLENLRLHVLAFSKSCHLPWASGLETLDSLGGVLEASGYS 141
|||

QY 121 TEWVALSRLOGLQDMLWQDLSPGC 146
|||
DB 142 TEWVALSRLOGLQDMLWQDLSPGC 167
|||

RESULT 3

OB PANTR STANDARD; PRT; 146 AA.

AC Q02750;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Pan troglodytes (Chimpanzee).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Pan.
OX NCBI_TaxID=9598;
RN [1]
RP SEQUENCE FROM N.A.
RA Schoner B., Basinski M.B., Smith D.P., Hsiung H.M., Zhang X.,
RA Rockey P.K., Rostock P.N.;
RT "Cloning of obese genes from different species: a comparison of the
gene structures and the sequences of the obese gene products,
leptin."
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.

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or send an email to license@isb-sib.ch).

DR EMBL; U96450; AAB54023.1; -;
DR HSP; P41159; 1AX8.
DR InterPro; IPR009079; 4_helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODom; PD005698; Leptin; 1.
KW Obesity.
FT DISULFID 96 146 By similarity.
SQ SEQUENCE 146 AA; 16058 MW; 02C42A06B554D55C CRC64;

Query Match 99.6%; Score 733; DB 1; Length 146;
Best Local Similarity 99.3%; Pred. No. 1.7e-59;
Matches 145; Conservative 1; Mismatches 0; Indels 0; Gaps 0;

QY 1 VPIQVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTLTKMDQTLAV 60
|||

DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Macaca mulatta (Rhesus macaque).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Cercopithecoidea;
OC Cercopithecoidea; Macaca.
OX NCBI_TaxID=9544;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RX MEDLINE=96411743; PubMed=8810296; DOI=10.1074/jbc.271.41.25327;
RA Hotta K., Gustafson T.A., Ortmeier H.K., Bodkin N.L., Nicolson M.A.,
Hansen B.C.;
RT "Regulation of obese (ob) mRNA and plasma leptin levels in rhesus
monkeys. Effects of insulin, body weight, and non-insulin-dependent
diabetes mellitus";
RL J. Biol. Chem. 271:25327-25331(1996).
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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CC -----
DR EMBL; U58492; AAC50730.1; -.
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18953 MW; E7D9F30628A5BB99 CRC64;
Query Match 91.3%; Score 672; DB 1; Length 167;
Best Local Similarity 91.1%; Pred. No. 8.4e-54;
Matches 133; Conservative 8; Mismatches 5; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSKMDQTLAV 60
DB 22 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSKMDQTLAI 81
QY 61 YQQLTSMPSRNVTQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSGGVLEASGYS 120
DB 82 YQQLTLPGRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167
RESULT 7
OB_FELCA STANDARD; PRT; 167 AA.
AC Q9N2C1;
DT 16-OCT-2001 (Rel. 40, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Felis silvestris catus (Cat).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Carnivora; Fissipedia; Felidae; Felis.
OX NCBI_TaxID=9685;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Sasaki N., Iwase M., Kimura K., Ohishi I., Saito M.;
RT "Molecular cloning of feline leptin cDNA";
RL Submitted (APR-2000) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.
CC -----
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or send an email to license@isb-sib.ch).
CC -----
DR EMBL; AB041360; BAA95481.1; -.
DR HSSP; P41159; IAX8.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR PRODOM; PD005698; Leptin; 1.
KW Obesity; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT SEQUENCE 167 AA; 18583 MW; 643720DBB0AB4B95 CRC64;
Query Match 86.8%; Score 639; DB 1; Length 167;
Best Local Similarity 86.3%; Pred. No. 9e-51;
Matches 126; Conservative 11; Mismatches 9; Indels 0; Gaps 0;
QY 1 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSKMDQTLAV 60
DB 22 VPIQKVQDDTKTLTKITVTRINDISHTQSVSSKQKVTGLDFIPGLHPILTSKMDQTLAI 81
QY 61 YQQLTSMPSRNVTQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSGGVLEASGYS 120
DB 82 YQQLTLPGRNVQISNDLENLRLDLHLVAFSKSCHLPWASGLTLDLSGGVLEASGYS 141
QY 121 TEVVALSRLOGLQDMLWQLDLSGPC 146
DB 142 TEVVALSRLOGLQDMLWQLDLSGPC 167
RESULT 8
Q6T8R8 PRELIMINARY; PRT; 146 AA.
AC Q6T8R8;
DT 05-JUL-2004 (TrEMBLrel. 27, Created)
DT 05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
DT 05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
DE Leptin (Fragment).
OS Bubalus bubalis (Domestic water buffalo).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bubalus.
OX NCBI_TaxID=89462;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Rajendran S., Shukla D.C., Saravanan B.C.;

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
DR EMBL; AY427959; AAR05862.1; -
DR HSSP; P41159; IAX8
DR GO; GO:0005576; C:extracellular; IEA.
DR GO; GO:0005179; F:hormone activity; IEA.
DR GO; GO:0007165; P:signal transduction; IEA.
DR InterPro; IPR009079; 4 helix_cytokine.
DR InterPro; IPR000065; Leptin.
DR Pfam; PF02024; Leptin; 1.
DR PRINTS; PR00495; LEPTIN.
DR ProDom; PD005698; Leptin; 1.
FT CHAIN 1 1
FT NON TER 1 1
SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 85.3%; Score 628; DB 2; Length 146;
Best Local Similarity 87.0%; Pred. No. 7.8e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIKQVDDTKTLIKITVTRINDISHTSQSSVKQVTGLDFIPGLHPILTLKMDQTLAV 60
DB 1 VPIKQVDDTKTLIKITVTRINDISHTSQSSVKQVTGLDFIPGLHPILTLKMDQTLAI 60

QY 61 YQOILTSMPNRVVIQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLGLGVLEASGYS 120
DB 61 YQOILTSMPNRVVIQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLGLGVLEASGYS 120

QY 121 TEVALSRLOGSQDMLQDLSPGC 146
DB 121 TEVALSRLOGSQDMLQDLSPGC 146

RESULT 9
OB BOVIN
ID OB BOVIN STANDARD; PRT; 167 AA
AC P05095; Q97918; Q95133; Q9TS29;
DT 01-OCT-1996 (Rel. 34, Created)
DT 01-OCT-1996 (Rel. 34, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB, OBS;
OS Bos taurus (Bovine).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
OC Bovinae; Bos.
OX NCBI_TaxID=9913;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=Liver;
RA Tellam R.L., Briscoe S., Vuocolo A.;
RL Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
RN [2]
RP SEQUENCE OF 22-167 FROM N.A.
RA Ji S., Spurlock M.E.;
RP "Partial cloning of bovine obesity gene."
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
RN [3]
RP SEQUENCE OF 22-167 FROM N.A.
RC TISSUE=white adipose tissue;
RA Kawakita Y., Abe H., Miyashige T.;
RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
RN [4]
RP SEQUENCE FROM N.A., AND VARIANTS CYS-25 AND VAL-80.
RC STRAIN=Jersey;
RX MEDLINE=20063685; PubMed=10594237;
RA Konfortov B.A., Licence V.E., Miller J.R.;
RT "Resequencing of DNA from a diverse panel of cattle reveals a high
RL level of polymorphism in both intron and exon."
RM Mamm. Genome 10:1142-1145(1999).
RN [5]
RP SEQUENCE FROM N.A., AND VARIANT CYS-25.
RA Liefers S.C.;
RT "Genotype effects of bovine leptin mutations on pre- and postpartum
leptin concentrations.";
RL Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE OF 46-145 FROM N.A.
RA Lien S., Sundvold H., Klungland H., Vaage D.I.;
RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
RL Anim. Genet. 28:245-245(1997).
RN [7]
RP SEQUENCE OF 60-146 FROM N.A.
RX MEDLINE=96269621; PubMed=8661738;
RA Pfister-Genskow M.A., Hayes H., Eggen A., Bishop M.D.;
RT "Chromosomal localization of the bovine obesity (OBS) gene.";
RL Mamm. Genome 7:398-399(1996).
RN [8]
RP SEQUENCE OF 1-48 FROM N.A.
RA Fitzsimmons C.J., Schmutz S.M.;
RT "Exon two of the bovine obese, leptin, gene.";
RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass.
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- SIMILARITY: Belongs to the leptin family.
CC
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CC
EMBL; U43943; AAA85906.1; -
EMBL; U50365; AAB61244.1; -
EMBL; U85793; AAB06579.1; -
EMBL; AB003143; BAA19750.1; -
EMBL; AJ132764; CAB64255.1; -
EMBL; AJ236854; CAB38018.1; -
EMBL; AJ512638; CAD54745.1; -
EMBL; AJ512639; CAD54745.1; JOINED.
EMBL; Y11369; CAA72197.1; -
EMBL; U43833; AAB18762.1; -
EMBL; AF120500; AAD23567.1; -
HSSP; P41159; IAX8.
InterPro; IPR009079; 4 helix_cytokine.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Obesity; Polymorphism; Signal.
FT SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT VARIANT 25 25 R -> C.
FT VARIANT 80 80 A -> V.
FT CONFLICT 25 25 R -> Q (in Ref. 2).
FT CONFLICT 166 166 G -> E (in Ref. 2).
SQ SEQUENCE 167 AA; 18716 MW; 94C666B3069E50B7 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
Best Local Similarity 87.0%; Pred. No. 9.3e-50;
Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIKQVDDTKTLIKITVTRINDISHTSQSSVKQVTGLDFIPGLHPILTLKMDQTLAV 60
DB 22 VPIKQVDDTKTLIKITVTRINDISHTSQSSVKQVTGLDFIPGLHPILTLKMDQTLAI 81

QY 61 YQOILTSMPNRVVIQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLGLGVLEASGYS 120
DB 82 YQOILTSMPNRVVIQISNDLENLRLDLHLVAFKSKCHLPWASGLTDLGLGVLEASGYS 141

Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
 DR EMBL; AY427959; AAR05862.1; -
 DR HSSP; P41159; 1AX8.
 DR GO; GO:0005576; C:extracellular; IEA.
 DR GO; GO:0005179; F:hormone activity; IEA.
 DR GO; GO:0007165; P:signal transduction; IEA.
 DR InterPro; IPR009079; 4_helix_cytokine; IEA.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; Leptin; 1.
 DR ProDom; PD005698; Leptin; 1.
 FT NON TER 1 1
 FT CHAIN 1 146
 SQ SEQUENCE 146 AA; 16069 MW; 1A745EE0851BD8CA CRC64;

Query Match 85.3%; Score 6281; Def 2; Length 146;
 Best Local Similarity 87.0%; Pred. No. 7.8e-50;
 Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKLTKITVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDOTLAV 60
 DB 1 VPIRKQDDTKLTKITVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDOTLAI 60
 QY 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 120
 DB 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 120
 QY 121 TEVALSRLOGLQDMLWQDLSPGC 146
 DB 121 TEVALSRLOGLQDMLWQDLSPGC 146

RESULT 9

OB BOVIN
 ID OB BOVIN
 AC P50595; O97918; STANDARD; PRT; 167 AA.
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 25-OCT-1996 (Rel. 34, Last sequence update)
 DE Leptin precursor (Obesity factor).
 GN Names=LEP; Synonyms=OB, OBS;
 OS Bos taurus (Bovine).
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
 OX NCBI_TaxID=9913;
 RP Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RA Tissue=Liver;
 RL Tissue=Liver;
 RN Submitted (JUN-1997) to the EMBL/GenBank/DBJ databases.
 RP Sequence of 22-167 FROM N.A.
 RA J. S., Spurlock M.E.;
 RT "Partial cloning of bovine obesity gene."
 RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
 RP Sequence of 22-167 FROM N.A.
 RC Tissue=White adipose tissue;
 RA Kawakita Y., Abe H., Miyashige T.;
 RL Submitted (APR-1997) to the EMBL/GenBank/DBJ databases.
 RP Sequence from N.A., AND VARIANTS CVS-25 AND VAL-80.
 RC STRAIN=Jersey;
 RX MEDLINE=20063685; PubMed=10594237;
 RA Konfortov B.A., Licence V.E., Miller J.R.;
 RT "Resequencing of DNA from a diverse panel of cattle reveals a high level of polymorphism in both intron and exon."
 RL Mamm. Genome 10:1142-1145 (1999).
 RP Sequence from N.A., AND VARIANT CVS-25.
 RA Liefers S.C.;
 RT "Genotype effects of bovine leptin mutations on pre- and postpartum

leptin concentrations."
 RT Submitted (OCT-2002) to the EMBL/GenBank/DBJ databases.
 RN [6]
 RP SEQUENCE OF 46-145 FROM N.A.
 RA Lien S., Sundvold H., Klungland H., Vaege D.I.;
 RT "Two novel polymorphisms in the bovine obesity gene (OBS).";
 RL Anim. Genet. 28:245-245 (1997).
 RN [7]
 RP SEQUENCE OF 60-146 FROM N.A.
 RA MEDLINE=96269621; PubMed=8661738;
 RT "Chromosomal localization of the bovine obesity (OBS) gene."
 RL Mamm. Genome 7:398-399 (1996).
 RN [8]
 RP SEQUENCE OF 1-48 FROM N.A.
 RA Fitzsimmons C.J., Schmutz S.M.;
 RT "Exon two of the bovine obese, leptin, gene."
 RL Submitted (JAN-1999) to the EMBL/GenBank/DBJ databases.
 CC -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
 CC -!- SIMILARITY: Belongs to the leptin family.
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 DR EMBL; U43943; AAA85906.1;
 DR EMBL; U50365; AAB61244.1;
 DR EMBL; U65793; AAB6579.1;
 DR EMBL; AB003143; BAA19750.1;
 DR EMBL; AJ132743; BAA19750.1;
 DR EMBL; AJ232764; CAB64255.1;
 DR EMBL; AJ236854; CAB38018.1;
 DR EMBL; AJ512638; CAD54745.1;
 DR EMBL; AJ512639; CAD54745.1;
 DR EMBL; Y11369; CA72197.1;
 DR EMBL; U43833; AAB18762.1;
 DR EMBL; AF120500; AAD23567.1;
 DR HSSP; P41159; 1AX8.
 DR InterPro; IPR009079; 4_helix_cytokine.
 DR Pfam; PF02024; Leptin; 1.
 DR PRINTS; PR00495; LEPTIN.
 DR ProDom; PD005698; Leptin; 1.
 KW Obesity; Polymorphism; Signal.
 FT SIGNAL 1 21 Potential.
 FT CHAIN 1 21 Leptin.
 FT DISULFID 22 167 By similarity.
 FT VARIANT 25 25 R -> C.
 FT CONFLICT 80 80 A -> V.
 FT CONFLICT 25 25 R -> Q (in Ref. 2).
 FT CONFLICT 166 166 G -> E (in Ref. 2).
 SQ SEQUENCE 167 AA; 18716 MW; 94C66B3069E50B7 CRC64;

Query Match 85.3%; Score 628; DB 1; Length 167;
 Best Local Similarity 87.0%; Pred. No. 9.3e-50;
 Matches 127; Conservative 10; Mismatches 9; Indels 0; Gaps 0;

QY 1 VPIQKQDDTKLTKITVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDOTLAV 60
 DB 1 VPIRKQDDTKLTKITVTRINDISHTQSVSSKQVGLDFPGLHPLLSKMDOTLAI 60
 QY 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 120
 DB 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 120
 QY 82 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 141
 DB 82 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAESKCHLPWASGLETLSLGVLEASGYS 141

121 TEVVALSRLQSLQDMLWQLDLSGPC 146
142 TEVVALSRLQSLQDMLWQLDLSGPC 167

RESULT 10

OB_PIG OB_PIG STANDARD; PRT; 167 AA.

Q29406; O19095; Q95251;
01-NOV-1997 (Rel. 35, Created)
01-NOV-1997 (Rel. 35, Last sequence update)
25-OCT-2004 (Rel. 45, Last annotation update)
Leptin precursor (Obesity factor).
Name=LEP; Synonyms=OB, OBS;
Sus scrofa (Pig).
Ox Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.
NCBI_TaxID=9823;
[1]
SEQUENCE FROM N.A.
RC TISSUE=Adipose tissue;
RA Louis C.F.;
RL Submitted (AUG-1996) to the EMBL/GenBank/DBJ databases.
[2]
SEQUENCE FROM N.A.
RP Ramey T.G., Yan X.;
RL Submitted (JUL-1996) to the EMBL/GenBank/DBJ databases.
[3]
SEQUENCE FROM N.A.
RP STRAIN=Landrace;
RC Robert C., Palin M.-F., Coulombe N., Roberge C., Silversides F.G.,
RA Benkel B.F., McKay R.M., Pelletier G.;
RL Submitted (SEP-1997) to the EMBL/GenBank/DBJ databases.
[4]
SEQUENCE FROM N.A.
RP Bidwell C.A., Ji S., Spurlock M.E.;
RL Submitted (JAN-1998) to the EMBL/GenBank/DBJ databases.
[5]
SEQUENCE FROM N.A.
RP STRAIN=Meishan;
RC Dai R., Li N., Hu X., Wu C.;
RA Submitted (MAR-1998) to the EMBL/GenBank/DBJ databases.
[6]
SEQUENCE FROM N.A.
RP McNeel R.L., Mersmann H.J.;
RL "Adipose tissue regulatory transcript expression in lean versus obese
pigs."
RT Submitted (OCT-1998) to the EMBL/GenBank/DBJ databases.
[7]
SEQUENCE FROM N.A.
RC STRAIN=Large white;
RP Soares M.A.M., Euclides R.F., Guimaraes S.E.F., Martins M.F.,
RA Lopes P.S.;
RL Submitted (JAN-2002) to the EMBL/GenBank/DBJ databases.
[8]
SEQUENCE OF 15-110 FROM N.A.
RP TISSUE=White adipose tissue;
RC MEDLINE=97009821; PubMed=8856925;
RX Neuenschwander S., Kettenberger G., Meijerink E., Jorg H.,
RA Stranzinger G.;
RL "Partial characterization of porcine obesity gene (OBS) and its
localization to chromosome 18 by somatic cell hybrids."
RT Anim. Genet. 27:275-278 (1996).
-!- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
-!- SUBCELLULAR LOCATION: Secreted (Probable).
-!- SIMILARITY: Belongs to the leptin family.

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Domest. Anim. Endocrinol. 14:295-303(1997).
 -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 -!- SUBCELLULAR LOCATION: Secreted (Probable).
 -!- SIMILARITY: Belongs to the leptin family.

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 EMBL; U84247; AB41786.1; -;
 EMBL; U62123; AB51033.1; -;
 HSSP; P41159; IAX8.
 InterPro; IPR009079; 4_helix_cytokine.
 Pfam; PF02024; Leptin; 1.
 PRINTS; PR00495; LEPTIN.
 PRODOM; PD005698; Leptin; 1.
 Obesity.
 DISULFID 96 146 By similarity.
 L -> H (in Ref. 2).
 A -> G (in Ref. 2).
 V -> L (in Ref. 2).
 CONFLICT 124 124
 CONFLICT 146 AA; 16053 MW; 19D54C53240968CA CRC64;
 SEQUENCE 146 AA; 16053 MW; 19D54C53240968CA CRC64;
 Query Match 84.8%; Score 624; DB 1; Length 146;
 Best Local Similarity 87.0%; Pred. No. 1.8e-49;
 Matches 127; Conservative 9; Mismatches 10; Indels 0; Gaps 0;
 Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQVTKGLDPIGLHPILTLKMDQTLAV 60
 Db 1 VPIRQVDDTKTLIKTIVTRINDISHTQSVSSKQVTKGLDPIGLHPILTLKMDQTLAI 60
 Qy 61 YQQLTSMPSERNVIOISNDLENLRLDLHLAFSKSCHLPWASGLTDLSDLGVLASGYS 120
 Db 61 YQQLIASLPSERNVIOISNDLENLRLDLHLAASKCPLPQVRALESLSGLVLEASLYS 120
 Qy 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 RESULT 12
 OB_MOUSE STANDARD; PRT; 167 AA.
 AC P41160;
 DT 01-FEB-1995 (Rel. 31, Created)
 DT 01-FEB-1995 (Rel. 31, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=Lept; Synonym=Ob;
 OS Mus musculus (Mouse).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
 NCBI_TaxID=10090;
 [1]
 SEQUENCE FROM N.A.
 MEDLINE=95075453; PubMed=7984236; DOI=10.1038/372425a0;
 Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
 "Positional cloning of the mouse obese gene and its human homologue";
 Nature 372:425-432(1994).
 [2]
 ERRATUM.
 Zhang Y., Proenca P., Maffei M., Barone M., Leopold L., Friedman J.M.;
 Nature 374:479-479(1995).
 [3]

SEQUENCE FROM N.A.
 STRAIN=C57BL/6J;
 Chehab F.F., Lim M.E.;
 Submitted (MAR-1995) to the EMBL/GenBank/DBJ databases.
 -!- FUNCTION: May function as part of a signaling pathway that acts to regulate the size of the body fat depot. An increase in the level of LEP may act directly or indirectly on the CNS to inhibit food intake and/or regulate energy expenditure as part of a homeostatic mechanism to maintain constancy of the adipose mass.
 -!- SUBCELLULAR LOCATION: Secreted (Probable).
 -!- DISEASE: Defects in Lep are the cause of profound obesity and type II diabetes.
 -!- SIMILARITY: Belongs to the leptin family.

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 EMBL; U18812; AAA64564.1; -;
 EMBL; U22421; AAA64213.1; -;
 PIR; S50863; LTMS.
 HSSP; P41159; IAX8.
 MGD; MGI:104663; Lep.
 GO; GO:0008083; F; growth factor activity; IDA.
 GO; GO:0005515; F; protein binding; IPI.
 GO; GO:0008206; P; bile acid metabolism; IDA.
 GO; GO:0045639; P; positive regulation of myeloid blood cell d. . .; IDA.
 GO; GO:0030300; P; regulation of cholesterol absorption; IDA.
 InterPro; IPR009079; 4_helix_cytokine.
 InterPro; IPR000065; Leptin.
 Pfam; PF02024; Leptin; 1.
 PRINTS; PR00495; LEPTIN.
 PRODOM; PD005698; Leptin; 1.
 Diabetes mellitus; Obesity; Signal.
 SIGNAL 1 21 potential.
 CHAIN 22 167 Leptin.
 DISULFID 117 167 By similarity.
 VARIANT 49 49 Missing (in 30% the clones).
 SQ SEQUENCE 167 AA; 18708 MW; D6783B6C76FD7116 CRC64;
 Query Match 84.1%; Score 619; DB 1; Length 167;
 Best Local Similarity 84.9%; Pred. No. 6.2e-49;
 Matches 124; Conservative 13; Mismatches 9; Indels 0; Gaps 0;
 Qy 1 VPIQKVDDTKTLIKTIVTRINDISHTQSVSSKQVTKGLDPIGLHPILTLKMDQTLAV 60
 Db 22 VPIQKVDDTKTLIKTIVTRINDISHTQSVSAKQVTKGLDPIGLHPILTLKMDQTLAV 81
 Qy 61 YQQLTSMPSERNVIOISNDLENLRLDLHLAFSKSCHLPWASGLTDLSDLGVLASGYS 120
 Db 82 YQQLVTLSPSNVLIQANDLENLRLDLHLAFSKCSLPQTSGLQKPSLDGLVLEASLYS 141
 Qy 121 TEVVALSRQGSQDMLWQLDLSFGC 146
 Db 142 TEVVALSRQGSQDMLWQLDLSFGC 167
 RESULT 13
 OB_RAT STANDARD; PRT; 167 AA.
 ID OB_RAT
 AC P50596;
 DT 01-OCT-1996 (Rel. 34, Created)
 DT 01-OCT-1996 (Rel. 34, Last sequence update)
 DT 25-OCT-2004 (Rel. 45, Last annotation update)
 DE Leptin precursor (Obesity factor).
 GN Name=Lept; Synonym=Ob;
 OS Rattus norvegicus (Rat).
 OC Eukaryota; Metazoa; Chordata; Vertebrata; Euteleostomi;
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.

NCBI_TaxID=10116;
[1]
SEQUENCE FROM N.A.
TSSUE=Testis;
MEDLINE=95386724; PubMed=7657834;
Ogawa Y., Masuzaki H., Isse N., Okazaki T., Mori K., Shigemoto M.,
Sato N., Tamura N., Hosoda K., Yoshimasa Y., Jingami H., Kawada T.,
Nakao K.;
"Molecular cloning of rat obese cDNA and augmented gene expression in
genetically obese Zucker fatty (fa/fa) rats";
J. Clin. Invest. 96:1647-1652(1995).
[2]
SEQUENCE FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Fat;
MEDLINE=95314614; PubMed=7794258;
Funahashi T., Shimomura I., Hiraoka H., Arai T., Takahashi M.,
Nakamura T., Nozaki S., Yamashita S., Takemura K., Tokunaga K.;
"Enhanced expression of rat obese (ob) gene in adipose tissues of
ventromedial hypothalamus (VMH)-lesioned rats";
Biochem. Biophys. Res. Commun. 211:469-475(1995).
[3]
SEQUENCE FROM N.A.
STRAIN=Leto, Oletif, and Zucker; TISSUE=Adipose tissue;
MEDLINE=95251725; PubMed=7733988;
Murakami T., Shima K.;
"Cloning of rat obese cDNA and its expression in obese rats.";
Biochem. Biophys. Res. Commun. 209:944-952(1995).
[4]
SEQUENCE OF 14-167 FROM N.A.
STRAIN=Sprague-Dawley; TISSUE=Fat;
Donohue P.A., Sivitz W.I., Bailey H.L.;
Submitted (FEB-1996) to the EMBL/GenBank/DBJ databases.
-1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of Lep may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass.
-1- SUBCELLULAR LOCATION: Secreted (Probable).
-1- SIMILARITY: Belongs to the leptin family.

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EMBL; D45862; BAA08296.1; -;
EMBL; S78586; AAB34657.2; -;
EMBL; D49653; BAA08529.1; -;
EMBL; U48849; AAC52514.1; -;
PIR; PC4034; LTRT.
HSP; P41159; IAX8.
RGD; 3000; Lep.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR000065; Leptin.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Obesity; Signal.
KW SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT CONFLICT 32 32 K -> T (in Ref. 2).
FT CONFLICT 163 163 L -> V (in Ref. 4).
SQ SEQUENCE 167 AA; 18866 MW; 3B5B563DA42EC84E CRC64;
Query Match 82.2%; Score 605; DB 1; Length 167;
Best Local Similarity 83.6%; Pred. No. 1.2e-47;
Matches 122; Conservative 13; Mismatches 11; Indels 0; Gaps 0;
Qy 1 VPIQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 60

Db 22 VPIHKVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 81
Qy 61 YQOILTSPGRNVQISNDLENLRDLHLVLAFLSKSCHLPWASGLTETDLSGGVLEASGYS 120
Db 82 YQOILTSLPQNVQLIAHDLNLRDLHLVLAFLSKSCHLPQTRGLQKPSLDGVLEASLYS 141
Qy 121 TEVVALSRLOQSLQDMQWLDLSPGC 146
Db 142 TEVVALSRLOQSLQDILQDLSPGC 167
RESULT 14
OB_CANFA STANDARD; PRT; 167 AA.
AC 002720; Q9TSG1;
15-JUL-1998 (Rel. 36, Created)
DT 16-OCT-2001 (Rel. 40, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LFP; Synonyms=OB;
OS Canis familiaris (Dog).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Euthera; Carnivora; Fissipedia; Canidae; Canis.
OX NCBI_TaxID=9615;
RN [1]
RP SEQUENCE FROM N.A.
RC TISSUE=White adipose tissue;
RA Iwase M., Sasaki N., Komagome R., Kimura K., Saito M.;
RT "Molecular cloning of canine leptin cDNA";
RL Submitted (DEC-1998) to the EMBL/GenBank/DBJ databases.
[2]
RN SEQUENCE OF 22-167 FROM N.A.
RC TISSUE=Adipose tissue;
RA Smith D.P., Zhang X., Hsiung H.M.;
RL Submitted (MAR-1997) to the EMBL/GenBank/DBJ databases.
CC -1- FUNCTION: May function as part of a signaling pathway that acts to
regulate the size of the body fat depot. An increase in the level
of LEP may act directly or indirectly on the CNS to inhibit food
intake and/or regulate energy expenditure as part of a homeostatic
mechanism to maintain constancy of the adipose mass (By
similarity).
CC -1- SUBCELLULAR LOCATION: Secreted (Probable).
CC -1- SIMILARITY: Belongs to the leptin family.

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EMBL; AB020986; BAA35129.1; -;
EMBL; U95642; AAB53654.1; -;
HSP; P41159; IAX8.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR000065; Leptin.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Obesity; Signal.
KW SIGNAL 1 21 Potential.
FT CHAIN 22 167 Leptin.
FT DISULFID 117 167 By similarity.
FT CONFLICT 148 148 N -> S (in Ref. 2).
SQ SEQUENCE 167 AA; 18654 MW; 9703CFBED2286A55 CRC64;
Query Match 81.0%; Score 596; DB 1; Length 167;
Best Local Similarity 82.2%; Pred. No. 8.1e-47;
Matches 120; Conservative 13; Mismatches 13; Indels 0; Gaps 0;
Qy 1 VPIQKQVDDTKTLIKTIVTRINDISHTQSVSSKQKVTGLDIPGLHPIILSKMDQTLAV 60

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Db 22 VPIKQVDDTKTLIKTIIVARINDISHTQSVSSKQKVAGLDFIPGLQPVLSRMDQTLAI 81
Qy 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAFAKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 82 YQOILNLSHSNRVQISNDLENLRLDLHLVLAFAKSCPLPRARGLETTFESLGGVLEASLYS 141
Qy 121 TEVVALSRLOGSLQDMLWQDLSPGC 146
Db 142 TEVVALNRLQAALQDMLRRLDLSPGC 167

Matches 120; Conservative 13; Mismatches 12; Indels 1; Gaps 1;
Qy 1 VPQKVODDTKTLIKTIIVTRINDISHTQSVSSKQKVAGLDFIPGLHPIILTLISKMDQTLAV 60
Db 19 VPQIFODDTKTLIKTIIVTRINDISHT-SVSAKQKVAGLDFIPGLHPIILTLISKMDQTLAV 77
Qy 61 YQOILTSMPNRNVIQISNDLENLRLDLHLVLAFAKSCHLPWASGLETLDSLGGVLEASGYS 120
Db 78 YQOVLTSPLSPONVLIQIANDLENLRLDLHLVLAFAKSCSLPQTSGLQKPESLDGVLEASLYS 137
Qy 121 TEVVALSRLOGSLQDMLWQDLSPGC 146
Db 138 TEVVALSRLOGSLQDILQDLISPEC 163
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Search completed: March 12, 2005, 05:03:39
Job time : 106.419 secs

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RESULT 15
OB_CHICK STANDARD; PRT; 163 AA.
AC 047164;
DT 15-JUL-1998 (Rel. 36, Created)
DT 15-JUL-1998 (Rel. 36, Last sequence update)
DT 25-OCT-2004 (Rel. 45, Last annotation update)
DE Leptin precursor (Obesity factor).
GN Name=LEP; Synonyms=OB;
OS Gallus gallus (Chicken).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Archosauria; Aves; Neognathae; Galliformes; Phasianidae; Phasianinae;
OC Gallus.
OX NCBI_TaxID=9031;
RN [1]
RP SEQUENCE FROM N.A.
RC STRAIN=Broiler; TISSUE=Liver;
RX MEDLINE=98201619; PubMed=9524275; DOI=10.1016/S0378-1119(97)00670-7;
RA Tacuis M., Chen J.W., Davidaud C., Dupont J., Derouet M., Simon J.;
RT "Cloning the chicken leptin gene.";
RL Gene 208:239-242(1998).
RN [2]
RP SEQUENCE FROM N.A.
RC STRAIN=Shaver; TISSUE=Adipose tissue, and Liver;
RA Ashwell C.M., Czerwinski S.M., McMurtry J.P.;
RL Submitted (AUG-1998) to the EMBL/GenBank/DBJ databases.
CC -!- FUNCTION: May function as part of a signaling pathway that acts to
CC regulate the size of the body fat depot. An increase in the level
CC of LEP may act directly or indirectly on the CNS to inhibit food
CC intake and/or regulate energy expenditure as part of a homeostatic
CC mechanism to maintain constancy of the adipose mass (By
CC similarity).
CC -!- SUBCELLULAR LOCATION: Secreted (Probable).
CC -!- TISSUE SPECIFICITY: Not exclusively localized in adipose tissue
CC but is also expressed in liver.
CC -!- SIMILARITY: Belongs to the leptin family.
```

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or send an email to license@isb-sib.ch).
-----
EMBL; AF012727; AAC60368.1; -
EMBL; AF082500; AAC32380.1; -
HSSP; P41159; IAX8.
InterPro; IPR009079; 4_helix_cytokine.
InterPro; IPR000065; Leptin.
Pfam; PF02024; Leptin; 1.
PRINTS; PR00495; LEPTIN.
ProDom; PD005698; Leptin; 1.
Obesity; Signal.
KW SIGNAL 1 18 Potential.
FT CHAIN 19 163 Leptin.
FT DISULFID 113 163 By similarity.
SQ SEQUENCE 163 AA; 18183 MW; 9F578DB2528B18FC CRC64;
Query Match 79.7%; Score 586.5; DB 1; Length 163;
Best Local Similarity 82.2%; Pred. NO. 5.9e-46;
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GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 04:53:33 ; Search time 32.5463 Seconds
(without alignments)
383.035 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWTGCGFLWLPYLVFVQ.....SRLOGLQDMLWQLDLSFGC 167

Scoring table:
BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 513545 seqs, 74649064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0
Maximum DB seq length: 2000000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued Patents AA:*
1: /cgn2_6/ptodata/1/iaa/5A COMB.pap:*
2: /cgn2_6/ptodata/1/iaa/5B COMB.pap:*
3: /cgn2_6/ptodata/1/iaa/6A COMB.pap:*
4: /cgn2_6/ptodata/1/iaa/6B COMB.pap:*
5: /cgn2_6/ptodata/1/iaa/PTUS COMB.pap:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pap:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	870	100.0	167	2	US-08-540-242A-4
2	870	100.0	167	2	US-08-347-563A-4
3	870	100.0	167	2	US-09-003-081-5
4	870	100.0	167	3	US-08-292-345B-4
5	870	100.0	167	3	US-08-648-262-5
6	870	100.0	167	3	US-08-648-263-5
7	870	100.0	167	3	US-08-485-942A-4
8	870	100.0	167	3	US-08-488-214A-4
9	870	100.0	167	3	US-08-488-208A-4
10	870	100.0	167	3	US-08-759-628-1
11	870	100.0	167	3	US-08-688-908-7
12	870	100.0	167	3	US-08-483-211A-4
13	870	100.0	167	3	US-08-488-223A-4
14	870	100.0	167	3	US-09-147-805-4
15	870	100.0	167	4	US-08-438-431A-4
16	870	100.0	167	4	US-08-488-225A-4
17	870	100.0	167	4	US-09-204-730B-4
18	870	100.0	167	4	US-09-316-393-4
19	870	100.0	167	4	US-09-377-081-17
20	870	100.0	167	4	US-09-686-647A-4
21	870	100.0	167	5	PCT-US96-01471-4
22	870	100.0	397	4	US-08-775-066-2
23	854.5	98.2	166	2	US-08-347-563A-6
24	854.5	98.2	166	3	US-08-292-345B-6
25	854.5	98.2	166	3	US-08-485-942A-6
26	854.5	98.2	166	3	US-08-488-214A-6
27	854.5	98.2	166	3	US-08-488-208A-6

28	854.5	98.2	166	3	US-08-483-211A-6	Sequence 6, Appli
29	854.5	98.2	166	3	US-08-488-223A-6	Sequence 6, Appli
30	854.5	98.2	166	4	US-08-438-431A-6	Sequence 6, Appli
31	854.5	98.2	166	4	US-08-488-225A-6	Sequence 6, Appli
32	854.5	98.2	166	4	US-09-204-730B-6	Sequence 6, Appli
33	854.5	98.2	166	4	US-09-316-393-6	Sequence 6, Appli
34	854.5	98.2	166	4	US-09-686-647A-6	Sequence 6, Appli
35	736	84.6	146	1	US-08-398-021-3	Sequence 3, Appli
36	736	84.6	146	2	US-08-788-943A-5	Sequence 3, Appli
37	736	84.6	146	2	US-08-823-104-3	Sequence 3, Appli
38	736	84.6	146	2	US-09-003-081-6	Sequence 6, Appli
39	736	84.6	146	3	US-08-648-262-6	Sequence 6, Appli
40	736	84.6	146	3	US-08-648-263-6	Sequence 6, Appli
41	736	84.6	146	3	US-08-914-375C-32	Sequence 32, Appli
42	736	84.6	146	4	US-09-172-644-1	Sequence 1, Appli
43	736	84.6	146	4	US-09-221-178-1	Sequence 1, Appli
44	736	84.6	146	4	US-09-200-919-1	Sequence 1, Appli
45	736	84.6	146	5	PCT-US96-00952-2	Sequence 2, Appli

ALIGNMENTS

RESULT 1
US-08-540-242A-4
; Sequence 4, Application US/08540242A
; Patent No. 5827734
; GENERAL INFORMATION:
; APPLICANT: Weigle, David S.
; APPLICANT: Kuijper, Joseph L.
; APPLICANT: Forstrom, John W.
; APPLICANT: Lehner, Joyce M.
; TITLE OF INVENTION: APPETITE SUPPRESSION FACTOR AND RELATED METHODS
; NUMBER OF SEQUENCES: 10
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: ZymoGenetics, Inc.
; STREET: 1201 Eastlake Avenue East
; CITY: Seattle
; STATE: WA
; COUNTRY: USA
; ZIP: 98102
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/540,242A
; FILING DATE:
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Parker, Gary E
; REGISTRATION NUMBER: 31,648
; REFERENCE/DOCKET NUMBER: 95-01C5
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 206-442-6673
; TELEFAX: 206-442-6678
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-540-242A-4

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWTGCGFLWLPYLVFVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWTGCGFLWLPYLVFVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60

QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSLP 120
Db |||||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db |||||||

RESULT 2

US-08-347-563A-4
; Sequence 4, Application US/08347563A
; Patent No. 5935810
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 38
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/347,563A
; FILING DATE: No. 5935810ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE: Human
US-08-347-563A-4

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db |||||||
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSLP 120
Db |||||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db |||||||

RESULT 3

US-09-003-081-5
; Sequence 5, Application US/09003081
; Patent No. 5968779
; GENERAL INFORMATION:
; APPLICANT: Campfield, Arthur Dr.
; APPLICANT: Devos, Rene Dr.
; APPLICANT: Guisez, Yves Dr.
; TITLE OF INVENTION: Recombinant Obese (OB) Proteins
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Hoffmann-La Roche, Inc.
; STREET: 340 Kingsland Street
; CITY: Nutley
; STATE: New Jersey
; COUNTRY: U.S.A.
; ZIP: 07110
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/003,081
; FILING DATE:
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/435,777
; FILING DATE:
; ATTORNEY/AGENT INFORMATION:
; NAME: Picut, Catherine A
; REGISTRATION NUMBER: 37419
; REFERENCE/DOCKET NUMBER: 9165
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (201) 235-4387
; TELEFAX: (201) 235-2363
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: not relevant
; TOPOLOGY: unknown
; MOLECULE TYPE: peptide
; HYPOTHEICAL: NO
; ANTI-SENSE: NO
US-09-003-081-5

Query Match 100.0%; Score 870; DB 2; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHGTLGFLWLPYLFVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db |||||||
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFSKSLP 120
Db |||||||
QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQDLSPGC 167
Db |||||||

RESULT 4

US-08-292-345B-4
; Sequence 4, Application US/08292345B
; Patent No. 6001968
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21

NAME: Kreisler, Lewis J
REGISTRATION NUMBER: 38522
REFERENCE/DOCKET NUMBER: RAN 4105/175-002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (201) 235-4387
TELEFAX: (201) 235-2363
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: not relevant
TOPOLOGY: unknown
MOLECULE TYPE: peptide
HYPOTHETICAL: NO
ANTI-SENSE: NO
US-08-648-263-5

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGFLWLPYLFVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGFLWLPYLFVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFAFSKCHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFAFSKCHLP 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 7

US-08-485-942A-4
Sequence 4, Application US/08485942A
Patent No. 6048837
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MARFEEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: OB POLYPEPTIDE AS MODULATORS OF BODY WEIGHT (AS
TITLE OF INVENTION: AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/485,942A
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2F
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-485-942A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGFLWLPYLFVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGFLWLPYLFVYQVAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFAFSKCHLP 120
DB 61 DFIPGLHPILTSLKMDQTLAVYQQILTSMPSRNVQISNDLENLRLDLLHLVLAFAFSKCHLP 120
QY 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDSLGGVLEASGYSTEVVALSRQSGSLQDMLWQLDLSGPC 167

RESULT 8

US-08-488-214A-4
Sequence 4, Application US/08488214A
Patent No. 6124439
GENERAL INFORMATION:
APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA,
APPLICANT: MARGHERITA MARFEEI, JEFFREY HALAAS, KETAN GAJIWALA, AND STEPHEN K. BURLE
TITLE OF INVENTION: OB POLYPEPTIDE ANTIBODIES AND METHOD OF MAKING
TITLE OF INVENTION: (AS AMENDED)
NUMBER OF SEQUENCES: 99
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent In Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,214A
FILING DATE: JUNE 7, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6124439ember 30, 1994
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP 2D
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-488-214A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

RESULT 9

US-08-488-208A-4
Sequence 4, Application US/08488208A
Patent No. 6124448
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/488,208A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6124448ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994

CLASSIFICATION: 514
ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-488-208A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

RESULT 10

US-08-759-628-1
Sequence 1, Application US/08759628
Patent No. 6225446
GENERAL INFORMATION:
APPLICANT: Altmann, Scott W.
APPLICANT: Rock, Fernando L.
APPLICANT: Bazan, J. Fernando
APPLICANT: Kastelein, Robert A.
TITLE OF INVENTION: MUTATIONAL VARIANTS OF MAMMALIAN PROTEINS
NUMBER OF SEQUENCES: 11
CORRESPONDENCE ADDRESS:
ADDRESSEE: DNAX Research Institute
STREET: 901 California Avenue
CITY: Palo Alto
STATE: California
COUNTRY: USA
ZIP: 94304-1104
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/759,628
FILING DATE: 05-DEC-1996
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 60/008,574
FILING DATE: 06-DEC-1995
ATTORNEY/AGENT INFORMATION:
NAME: Ching, Edwin P.
REGISTRATION NUMBER: 34,090
REFERENCE/DOCKET NUMBER: DX0552Q
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-852-9196
TELEFAX: 415-496-1200

INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-759-628-1

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGFLMWPLYFYVQAVPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGFLMWPLYFYVQAVPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPSRNVQISNDLENLDLHLVLAFSKSCHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPSRNVQISNDLENLDLHLVLAFSKSCHLP 120
QY 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 11
US-08-688-908-7
Sequence 7, Application US/08688908
Patent No. 6297027
GENERAL INFORMATION:
APPLICANT: Spurlock, Michael E.
TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
TITLE OF INVENTION: SEQUENCES CODING THEREFOR AND USES THEREOF
NUMBER OF SEQUENCES: 8
CORRESPONDENCE ADDRESS:
ADDRESSEE: WYTHE HIRSCHBOECK DUDEK S.C.
STREET: Suite 2100 111 East Wisconsin Avenue
CITY: Milwaukee
STATE: Wisconsin
COUNTRY: USA
ZIP: 53202

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/688,908
FILING DATE: 31-JUL-1996
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Plotcher, Gary R.
REGISTRATION NUMBER: 27,830
REFERENCE/DOCKET NUMBER: PM-8808
TELECOMMUNICATION INFORMATION:
TELEPHONE: 414-273-2100
TELEFAX: 414-223-5000
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-688-908-7

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGFLMWPLYFYVQAVPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
|||||

DB 1 MHWGTLGFLMWPLYFYVQAVPIQKVQDDTKTIKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPSRNVQISNDLENLDLHLVLAFSKSCHLP 120
DB 61 DFIPGLHPILTLTKMDQTLAVYQOILTSMPSRNVQISNDLENLDLHLVLAFSKSCHLP 120
QY 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSLGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSGPC 167

RESULT 12
US-08-483-211A-4
Sequence 4, Application US/08483211A
Patent No. 6309853
GENERAL INFORMATION:
APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
TITLE OF INVENTION: NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC
TITLE OF INVENTION: USES THEREOF
NUMBER OF SEQUENCES: 98
CORRESPONDENCE ADDRESS:
ADDRESSEE: Klauber & Jackson
STREET: 411 Hackensack Avenue
CITY: Hackensack
STATE: New Jersey
COUNTRY: USA
ZIP: 07601

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patent in Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/483,211A
FILING DATE: 07-JUN-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/485,943
FILING DATE: June 7, 1995
APPLICATION NUMBER: 08/438,431
FILING DATE: May 10, 1995
CLASSIFICATION: 514

PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/347,563
FILING DATE: No. 6309853ember 30, 1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/292,345
FILING DATE: August 17, 1994
CLASSIFICATION: 514

ATTORNEY/AGENT INFORMATION:
NAME: Jackson Esq., David A.
REGISTRATION NUMBER: 26,742
REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
TELECOMMUNICATION INFORMATION:
TELEPHONE: 201 487-5800
TELEFAX: 201 343-1684
TELEX: 133521
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 167 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide
ORIGINAL SOURCE: Human
US-08-483-211A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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DB 1 MHWGTLGFLWLPYLFYVQVPIQKVQDDTKTLTKTIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSCHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSCHLP 120
QY 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
DB 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167

RESULT 13
US-08-488-223A-4
; Sequence 4, Application US/08488223A
; Patent No. 6350730
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THE
; NUMBER OF SEQUENCES: 98
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/488,223A
; FILING DATE: 07-Jun-1995
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/485,943
; FILING DATE: <Unknown>
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6350730ember 30, 1994
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP21
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-08-488-223A-4

Query Match 100.0%; Score 870; DB 3; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPSRNVQISNDLENRLDLHLVLAFAFSKSCHLP 120
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DB 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167
RESULT 14
US-09-147-805-4
; Sequence 4, Application US/09147805
; Patent No. 6399745
; GENERAL INFORMATION:
; APPLICANT: ERTL, Johann
; PREIBISCH, Gerald
; MUELLER, Guenter
; TITLE OF INVENTION: USE OF LEPTIN ANTAGONISTS FOR TREATING
; INSULIN RESISTANCE IN TYPE II DIABETES
; NUMBER OF SEQUENCES: 7
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: FOLEY & LARDNER
; STREET: 3000 K Street, N.W.
; CITY: Washington
; STATE: D.C.
; COUNTRY: U.S.A.
; ZIP: 20007-5109
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patent in Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/147,805
; FILING DATE: 14-Apr-1999
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: WO PCT/EP97/05035
; FILING DATE: 15-SEP-1997
; APPLICATION NUMBER: DE 196 38 487.7
; FILING DATE: 20-SEP-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Granados, Patricia D.
; REGISTRATION NUMBER: 33,683
; REFERENCE/DOCKET NUMBER: 03e083/0200
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: (202) 672-5300
; TELEFAX: (202) 672-5399
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
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DB 121 WASGLETLDSLGGLVLEASGYSTEVVALSRLOGLSQDMLWQDLSPGC 167

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; Sequence 4, Application US/08438431A
; Patent No. 6429290
; GENERAL INFORMATION:
; APPLICANT: JEFFREY M. FRIEDMAN, YIYING ZHANG, RICARDO PROENCA, MARGHERITA MAFFEI,
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC ACIDS AND PR
; NUMBER OF SEQUENCES: 99
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/438,431A
; FILING DATE: May 10, 1995
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/347,563
; FILING DATE: No. 6429290ember 30, 1994
; CLASSIFICATION: 514
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
; FILING DATE: August 17, 1994
; CLASSIFICATION: 514
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087 CIP1
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE: Human
; US-08-438-431A-4

Query Match 100.0%; Score 870; DB 4; Length 167;
Best Local Similarity 100.0%; Pred. No. 9.3e-88;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGCFLLWLPYLFVQVAPVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
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Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSIQDMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRQGSIQDMLWQLDLSFGC 167

Search completed: March 12, 2005, 05:05:39
Job time : 33.5463 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: March 12, 2005, 05:03:46 ; Search time 93.9042 Seconds
(without alignments)
586.599 Million cell updates/sec

Title: US-10-049-182-4
Perfect score: 870
Sequence: 1 MHWGTLGFLWLPYFVQ.....SRLOGSLQDMLWQLDLSFGC 167

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Gapop 10.0 , Gapext 0.5

Searched: 1396920 seqs, 329844858 residues

Total number of hits satisfying chosen parameters: 1396920

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : Published Applications AA:*

- 1: /cgn2_6/ptodata/1/pubpaa/US07_PUBCOMB.pep.*
- 2: /cgn2_6/ptodata/1/pubpaa/PCT_NEW_PUB.pep.*
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- 20: /cgn2_6/ptodata/1/pubpaa/US60_PUBCOMB.pep.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	870	100.0	167	9	US-09-736-084-4
2	870	100.0	167	9	US-09-928-522-7
3	870	100.0	167	9	US-09-789-306-3
4	870	100.0	167	9	US-09-804-409A-11
5	870	100.0	167	10	US-09-316-393-4
6	870	100.0	167	15	US-10-440-464-67
7	870	100.0	167	15	US-10-458-334-17
8	870	100.0	167	17	US-10-698-510-17
9	870	100.0	396	9	US-09-859-361-2
10	870	100.0	396	9	US-09-859-361-5
11	870	100.0	397	8	US-08-779-457-47
12	870	100.0	397	17	US-10-921-710-47
13	870	100.0	399	9	US-09-859-361-7

14	870	100.0	401	9	US-09-859-361-9
15	854.5	98.2	166	9	US-09-736-084-6
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17	767	88.2	167	9	US-09-789-306-5
18	736	84.6	146	14	US-10-191-377-1
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20	736	84.6	146	15	US-10-419-058-2
21	736	84.6	146	15	US-10-467-114-1
22	736	84.6	146	16	US-10-622-998-1
23	736	84.6	146	16	US-10-658-834A-211
24	736	84.6	146	16	US-10-468-496-1
25	736	84.6	146	16	US-10-872-198-127
26	736	84.6	146	17	US-10-623-189-1
27	736	84.6	374	15	US-10-679-999-15
28	736	84.6	374	15	US-10-679-999-18
29	736	84.6	379	15	US-10-679-999-9
30	736	84.6	379	15	US-10-679-999-12
31	734	84.4	146	16	US-10-658-834A-666
32	734	84.4	146	16	US-10-658-834A-672
33	734	84.4	146	16	US-10-658-834A-677
34	734	84.4	146	16	US-10-658-834A-683
35	733	84.3	146	16	US-10-658-834A-665
36	733	84.3	146	16	US-10-658-834A-671
37	733	84.3	146	16	US-10-658-834A-673
38	733	84.3	146	16	US-10-658-834A-676
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41	731	84.0	146	16	US-10-658-834A-674
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43	731	84.0	146	16	US-10-658-834A-679
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45	731	84.0	147	9	US-09-366-133-6

ALIGNMENTS

RESULT 1

US-09-736-084-4
; Sequence 4, Application US/09736084
; Patent No. US20020107211A1
; GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING
NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent In Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,084

FILING DATE: 13-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/438,431

FILING DATE: May 10, 1995

APPLICATION NUMBER: 08/347,563

FILING DATE: No. US20020107211A1

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

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;
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human ob polypeptide
; ORIGINAL SOURCE:
; SEQUENCE DESCRIPTION: SEQ ID NO: 4:
US-09-736-084-4
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Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSFGC 167
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; RESULT 2
; US-09-928-522-7
; Sequence 7, Application US/09928522
; Patent No. US20020110857A1
; GENERAL INFORMATION:
; APPLICANT: Spurlock, Michael E.
; TITLE OF INVENTION: BOVINE LEPTIN PROTEIN, NUCLEIC ACID
; SEQUENCES CODING THEREFOR AND USES THEREOF
; NUMBER OF SEQUENCES: 8
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: WHYTE HIRSCHBOECK DUDEK S.C.
; STREET: Suite 2100 111 East Wisconsin Avenue
; CITY: Milwaukee
; STATE: Wisconsin
; COUNTRY: USA
; ZIP: 53202
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/928,522
; FILING DATE: 13-Aug-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: US/08/688,908
; FILING DATE: 31-JUL-1996
; ATTORNEY/AGENT INFORMATION:
; NAME: Plottecher, Gary R.
; REGISTRATION NUMBER: 27,830
; REFERENCE/DOCKET NUMBER: PM-8808
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 414-223-2100
; TELEFAX: 414-223-5000
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: <Unknown>
; TOPOLOGY: linear
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; Query Match 100.0%; Score 870; DB 9; Length 167;
; Best Local Similarity 100.0%; Pred. No. 2.7e-84;
; Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; QY 1 MHWGTLGGLWLPYLFYVQVPIQKVQDDTKLTKTIIVTRINDISHTQSVSSKQKVTGL 60
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Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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QY 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSFGC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGLQDMLWQLDLSFGC 167
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; RESULT 3
; US-09-789-306-3
; Sequence 3, Application US/09789306
; Patent No. US20020142456A1
; GENERAL INFORMATION:
; APPLICANT: Hernday, Nataasha
; TITLE OF INVENTION: Canine OB Protein Compositions and
; METHODS
; NUMBER OF SEQUENCES: 5
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Amgen Inc.
; STREET: One Amgen Center Drive
; CITY: Thousand Oaks
; STATE: California
; COUNTRY: U.S.A.
; ZIP: 91320
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: Patentin Release #1.0, Version #1.30
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/789,306
; FILING DATE: 20-Feb-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/609,408
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Eggert, Joan D.
; REFERENCE/DOCKET NUMBER: A-387
; INFORMATION FOR SEQ ID NO: 3:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; FEATURE:
; NAME/KEY: Leader Sequence
; LOCATION: -21 to -1
; SEQUENCE DESCRIPTION: SEQ ID NO: 3:
US-09-789-306-3
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Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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; Sequence 11, Application US/09804409A
; Patent No. US20020155100A1
; GENERAL INFORMATION:
; APPLICANT: KIEFFER, TIMOTHY J.
; APPLICANT: CHEUNG, ANTHONY T.
; TITLE OF INVENTION: COMPOSITIONS AND METHODS FOR REGULATED PROTEIN
; TITLE OF INVENTION: EXPRESSION IN GUT
; FILE REFERENCE: 029996/027 8721
; CURRENT APPLICATION NUMBER: US/09/804,409A
; CURRENT FILING DATE: 2001-03-12
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 11
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-804-409A-11

Query Match 100.0%; Score 870; DB 9; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGGLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGGLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVALSRLOGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVALSRLOGSLQDMLWQLDLSGPC 167

RESULT 5
US-09-316-393-4
; Sequence 4, Application US/09316393
; Publication No. US20030040039A1
; GENERAL INFORMATION:
; APPLICANT: THE ROCKEFELLER UNIVERSITY
; TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING NUCLEIC
; TITLE OF INVENTION: ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC USES THEREOF
; NUMBER OF SEQUENCES: 21
; CORRESPONDENCE ADDRESS:
; ADDRESS: Klauber & Jackson
; STREET: 411 Hackensack Avenue
; CITY: Hackensack
; STATE: New Jersey
; COUNTRY: USA
; ZIP: 07601
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: PatentIn Release #1.0, Version #1.25
; CURRENT APPLICATION DATA:
; FILING DATE:
; APPLICATION NUMBER: US/09/316,393
; CLASSIFICATION:
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/292,345
```

```
; FILING DATE: August 17, 1994
; ATTORNEY/AGENT INFORMATION:
; NAME: Jackson Esq., David A.
; REGISTRATION NUMBER: 26,742
; REFERENCE/DOCKET NUMBER: 600-1-087
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 201 487-5800
; TELEFAX: 201 343-1684
; TELEX: 133521
; INFORMATION FOR SEQ ID NO: 4:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 167 amino acids
; TYPE: amino acid
; TOPOLOGY: linear
; MOLECULE TYPE: protein
; DESCRIPTION: Human Ob protein
; ORIGINAL SOURCE: Human
US-09-316-393-4

Query Match 100.0%; Score 870; DB 10; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGGLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
DB 1 MHWGTLGGLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
DB 61 DFIPGLPILTLTKMDQTLAVYQQILTSMPNRNVIQISNDLENLRLDLHLVLAFSKSHLP 120
QY 121 WASGLETLDLSGGVLEASGYSTEVALSRLOGSLQDMLWQLDLSGPC 167
DB 121 WASGLETLDLSGGVLEASGYSTEVALSRLOGSLQDMLWQLDLSGPC 167

RESULT 6
US-10-440-464-67
; Sequence 67, Application US/10440464
; Publication No. US20040018528A1
; GENERAL INFORMATION:
; APPLICANT: DEPRIMO, SAMUEL
; APPLICANT: O'FARRELL, ANNE-MARIE
; APPLICANT: MORIMOTO, ALYSSA
; APPLICANT: SMOLICH, BEVERLY
; APPLICANT: MANNING, WILLIAM
; APPLICANT: WALTER, SARAH
; APPLICANT: CHERRINGTON, JULIE
; APPLICANT: SCHILLING, JIM
; TITLE OF INVENTION: NOVEL BIOMARKERS OF TYROSINE KINASE INHIBITOR EXPOSURE
; TITLE OF INVENTION: AND ACTIVITY IN MAMMALS
; FILE REFERENCE: 038602/1592
; CURRENT APPLICATION NUMBER: US/10/440,464
; CURRENT FILING DATE: 2003-05-19
; PRIOR APPLICATION NUMBER: 60/380,872
; PRIOR FILING DATE: 2002-05-17
; PRIOR APPLICATION NUMBER: 60/448,922
; PRIOR FILING DATE: 2003-02-24
; PRIOR APPLICATION NUMBER: 60/448,874
; PRIOR FILING DATE: 2003-02-24
; NUMBER OF SEQ ID NOS: 185
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 67
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-440-464-67

Query Match 100.0%; Score 870; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 MHWGTLGGLWLPYLFYVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
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Db 1 MHWGTLGFLWLPYLFYVQAVPIQVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167
121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167

RESULT 7

US-10-458-334-17
; Sequence 17, Application US/10458334
; Publication No. US20040043932A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia G
; APPLICANT: Lee, Daniel W.
; APPLICANT: Leinung, Matthew C.
; TITLE OF INVENTION: Leptin-Related Peptides
; FILE REFERENCE: AMC-1 Leptin Peptides (19705-001)
; CURRENT APPLICATION NUMBER: US/10/458,334
; CURRENT FILING DATE: 2003-06-09
; PRIOR APPLICATION NUMBER: US/09/377,081
; PRIOR FILING DATE: 1999-08-19
; PRIOR APPLICATION NUMBER: U.S.N. 60/097,457
; PRIOR FILING DATE: 1998-08-21
; NUMBER OF SEQ ID NOS: 18
; SOFTWARE: PatentIn Ver. 2.0
; SEQ ID NO 17
; LENGTH: 167
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-458-334-17

Query Match 100.0%; Score 870; DB 15; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGFLWLPYLFYVQAVPIQVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
QY 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167
121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167

RESULT 8

US-10-698-510-17
; Sequence 17, Application US/10698510
; Publication No. US20050049193A1
; GENERAL INFORMATION:
; APPLICANT: Grasso, Patricia
; APPLICANT: Lee, Daniel
; APPLICANT: Leinung, Matthew
; TITLE OF INVENTION: Leptin Related Peptides
; FILE REFERENCE: 19705-001CIP
; CURRENT APPLICATION NUMBER: US/10/698,510
; CURRENT FILING DATE: 2003-10-31
; PRIOR APPLICATION NUMBER: US 60/422,723
; PRIOR FILING DATE: 2002-10-31
; PRIOR APPLICATION NUMBER: US 09/377,081
; PRIOR FILING DATE: 1999-08-19
; NUMBER OF SEQ ID NOS: 42
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 17
; LENGTH: 167

; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-698-510-17
Query Match 100.0%; Score 870; DB 17; Length 167;
Best Local Similarity 100.0%; Pred. No. 2.7e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY 1 MHWGTLGFLWLPYLFYVQAVPIQVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQVQDDTKTLIKITIVTRINDISHTQSVSSKQKVTGL 60
QY 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
Db 61 DFIPGLHPILTLTKMDQTLAVYQIILTSMPNRNVIQISNDLENLRDLHLVLAFSKCHLP 120
QY 121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167
121 WASGLETLDSLGVLVLEASGYSTEVVALSRLOGSLQDMLWQLDLSFGC 167

RESULT 9

US-09-859-361-2
; Sequence 2, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; APPLICANT: Chapman, Conrad
; APPLICANT: Clinkenbeard, Helen
; APPLICANT: Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 2:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 2:
US-09-859-361-2

Query Match 100.0%; Score 870; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
RESULT 10
US-09-859-361-5
; Sequence 5, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinkenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: PASCSEQ for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 5:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 396 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 5:
US-09-859-361-5
Query Match 100.0%; Score 870; DB 9; Length 396;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120

Qy 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
RESULT 11
US-08-779-457-47
; Sequence 47, Application US/08779457
; Publication No. US20020193571A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kyung, Jin Kim
; APPLICANT: Matthews, William
; APPLICANT: Rodriguez, Maria L.
; TITLE OF INVENTION: WSX RECEPTOR AGONIST ANTIBODIES
; NUMBER OF SEQUENCES: 51
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Genentech, Inc.
; STREET: 460 Point San Bruno Blvd
; CITY: South San Francisco
; STATE: California
; COUNTRY: USA
; ZIP: 94080
; COMPUTER READABLE FORM:
; MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
; COMPUTER: IBM PC compatible
; OPERATING SYSTEM: PC-DOS/MS-DOS
; SOFTWARE: WinPatIn (Genentech)
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/08/779,457
; FILING DATE:
; CLASSIFICATION: 435
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/667197
; FILING DATE: 06/20/96
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/585005
; FILING DATE: 01/08/96
; ATTORNEY/AGENT INFORMATION:
; NAME: Lee, Wendy M.
; REGISTRATION NUMBER: 40,378
; REFERENCE/DOCKET NUMBER: P0986P2
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 415/225-1994
; TELEFAX: 415/952-9881
; TELEX: 910/371-7168
; INFORMATION FOR SEQ ID NO: 47:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 397 amino acids
; TYPE: Amino Acid
; TOPOLOGY: Linear
; US-08-779-457-47
Query Match 100.0%; Score 870; DB 8; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Db 1 MHWGTLGFLWLPYLFYVQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSCKVTGL 60
Qy 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTLKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
Db 121 WASGLETLDLSGGVLEASGYSTEVVALSRLOGSLODMLWQDLSPGC 167
RESULT 12
US-10-921-710-47

; Sequence 47, Application US/10921710
; Publication No. US20050019325A1
; GENERAL INFORMATION:
; APPLICANT: Carter, Paul J.
; APPLICANT: Chiang, Nancy Y.
; APPLICANT: Kim, Kyung Jin
; APPLICANT: Matthews, William
; TITLE OF INVENTION: METHODS FOR IDENTIFYING ANTIBODIES THAT
; DECREASE BODY WEIGHT, FAT-DEPOT WEIGHT OR FOOD INTAKE IN AN
; OBESE ANIMAL
; FILE REFERENCE: GENENT.53CP2C1
; CURRENT APPLICATION NUMBER: US/10/921,710
; CURRENT FILING DATE: 2004-08-18
; PRIOR APPLICATION NUMBER: 08/779457
; PRIOR FILING DATE: 1997-01-07
; PRIOR APPLICATION NUMBER: 60/064855
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/585005
; PRIOR FILING DATE: 1996-01-08
; PRIOR APPLICATION NUMBER: 08/667197
; PRIOR FILING DATE: 1996-06-20
; NUMBER OF SEQ ID NOS: 51
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 47
; LENGTH: 397
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-921-710-47

Query Match 100.0%; Score 870; DB 17; Length 397;
Best Local Similarity 100.0%; Pred. No. 8.9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLCGFLWLPYFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLCGFLWLPYFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLODMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLODMLWQLDLSFGC 167

RESULT 13
US-09-859-361-7
; Sequence 7, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinckenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001

; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202
; TELECOMMUNICATION INFORMATION:
; TELEPHONE: 610-270-5096
; TELEFAX: 610-270-5090
; TELEX: <Unknown>
; INFORMATION FOR SEQ ID NO: 7:
; SEQUENCE CHARACTERISTICS:
; LENGTH: 399 amino acids
; TYPE: amino acid
; STRANDEDNESS: single
; TOPOLOGY: linear
; SEQUENCE DESCRIPTION: SEQ ID NO: 7:
US-09-859-361-7

Query Match 100.0%; Score 870; DB 9; Length 399;
Best Local Similarity 100.0%; Pred. No. 9e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLCGFLWLPYFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLCGFLWLPYFVQAVPIQKVQDDTKLIKTIIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLLHLVLAFSKSCHLP 120
Db 61 DFIPGLHPILTSKMDQTLAVYQQILTSMPSRNVIQISNDLENLRLDLLHLVLAFSKSCHLP 120
Qy 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLODMLWQLDLSFGC 167
Db 121 WASGLETLDSLGGVLEASGYSTEVVALSRLOGSLODMLWQLDLSFGC 167

RESULT 14
US-09-859-361-9
; Sequence 9, Application US/09859361
; Patent No. US20020058311A1
; GENERAL INFORMATION:
; APPLICANT: Browne, Michael
; Chapman, Conrad
; Clinckenbeard, Helen
; Robinson, Jeffrey
; TITLE OF INVENTION: Chimeric Leptin Fused to Immunoglobulin
; Domain and Use
; NUMBER OF SEQUENCES: 9
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: SmithKline Beecham Corporation
; STREET: 709 Swedeland Road
; CITY: King of Prussia
; STATE: PA
; COUNTRY: USA
; ZIP: 19406
; COMPUTER READABLE FORM:
; MEDIUM TYPE: Diskette
; COMPUTER: IBM Compatible
; OPERATING SYSTEM: DOS
; SOFTWARE: FastSeq for Windows Version 2.0
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/09/859,361
; FILING DATE: 17-May-2001
; CLASSIFICATION: <Unknown>
; PRIOR APPLICATION DATA:
; APPLICATION NUMBER: 08/981,783
; FILING DATE: <Unknown>
; ATTORNEY/AGENT INFORMATION:
; NAME: Baumeister, Kirk
; REGISTRATION NUMBER: 33,833
; REFERENCE/DOCKET NUMBER: P31202

TELECOMMUNICATION INFORMATION:
TELEPHONE: 610-270-5096
TELEFAX: 610-270-5090
TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 401 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO: 9:
US-09-859-361-9

Query Match 100.0%; Score 870; DB 9; Length 401;
Best Local Similarity 100.0%; Pred. No. 9.1e-84;
Matches 167; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
Qy 1 MHWGTLGFLWLPYLFVYQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVYQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Qy 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSKCHLP 120
Db 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSKCHLP 120
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167
Db 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167

RESULT 15

US-09-736-084-6
Sequence 6, Application US/09736084
Patent No. US20020107211A1

GENERAL INFORMATION:

APPLICANT: THE ROCKEFELLER UNIVERSITY
TITLE OF INVENTION: MODULATORS OF BODY WEIGHT, CORRESPONDING

NUCLEIC ACIDS AND PROTEINS, AND DIAGNOSTIC AND THERAPEUTIC

NUMBER OF SEQUENCES: 98

CORRESPONDENCE ADDRESS:

ADDRESSEE: Klauber & Jackson

STREET: 411 Hackensack Avenue

CITY: Hackensack

STATE: New Jersey

COUNTRY: USA

ZIP: 07601

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patent in Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/09/736,084

FILING DATE: 13-Dec-2000

CLASSIFICATION: <Unknown>

PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/438,431

FILING DATE: May 10, 1995

APPLICATION NUMBER: 08/347,563

FILING DATE: No. US20020107211A1, November 30, 1994

APPLICATION NUMBER: 08/292,345

FILING DATE: August 17, 1994

ATTORNEY/AGENT INFORMATION:

NAME: Jackson Esq., David A.

REGISTRATION NUMBER: 26,742

REFERENCE/DOCKET NUMBER: 600-1-087 CIP2I

TELECOMMUNICATION INFORMATION:

TELEPHONE: 201 487-5800

TELEFAX: 201 343-1684

TELEX: 133521

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 166 amino acids

TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
DESCRIPTION: Human ob polypeptide lacking Gln at position
ORIGINAL SOURCE:
ORGANISM: Human
SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-736-084-6

Query Match 99.2%; Score 854.5; DB 9; Length 166;
Best Local Similarity 99.4%; Pred. No. 1.2e-82;
Matches 166; Conservative 0; Mismatches 0; Indels 1; Gaps 1;

Qy 1 MHWGTLGFLWLPYLFVYQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 60
Db 1 MHWGTLGFLWLPYLFVYQAVPIQKVQDDTKTLIKTIVTRINDISHTQSVSSKQKVTGL 59
Qy 61 DFIFGLHPILTLTKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSKCHLP 120
Db 60 DFIFGLHPILTLTKMDQTLAVYQOILTSMPSRNVIQISNDLENLRLDLHLVLAFAKSKCHLP 119
Qy 121 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 167
Db 120 WASGLETLDLSLGGVLEASGYSTEVVALSRQGSLODMLWQLDLSFGC 166

Search completed: March 12, 2005, 05:21:03

Job time : 94.9042 secs

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